



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 163765

TO: **Phuong Bui**  
Art Unit: **1638**  
Location: **REM 2C18/2A15**  
Serial Number: **107734698**

**Wednesday, August 31, 2005**

From: **Beverly Shears**  
Location: **Biotech-Chem Library**  
**REM 1A54**  
Phone: **571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 18:36:04 ; Search time 5037.58 Seconds  
(without alignments)  
11220.746 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
Sequence: 1 AGCCAAAGCCCCACTCAACCA.....CAAAAGAAATGTCGAAGTT 1485

Scoring table: IDENTITY NUC  
Gap 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	819.6	55.2	1191	9	CL970400	CL970400 OsIFCC041
2	813.4	54.8	1191	9	CL958884	CL958884 OsIFCC036
3	748	50.4	772	6	CA800424	CA800424 eaui15h12.
4	744.6	50.1	1912	3	AY109333	AY109333 Zea mays
5	736.8	49.6	740	7	CK606439	CK606439 gmrhww6-
6	729	49.1	775	4	BI968543	BI968543 GM830005B
7	716.6	48.3	760	2	BE660984	BE660984 469 GmaxS
8	706.8	47.6	969	7	CK276743	CK276743 EST722821
9	701.8	47.3	967	7	CK290599	CK290599 EST753313
10	698.4	47.0	1400	3	CNS0A7B6	EX822853 Arabidops
11	695.4	46.8	954	3	CK263461	CK263461 EST709539
12	690.4	46.5	1498	3	CNS0A7V6	EX823645 Arabidops
13	685	46.1	1235	6	CB330707	CB330707 SPST664
14	673.6	45.4	1008	7	CK269428	CK269428 EST715506
15	669.6	45.1	979	7	CK274045	CK274045 EST720123
16	667	44.9	946	7	CK263343	CK263343 EST709421
17	658.8	44.4	670	7	CF806716	CF806716 psHB015XD
18	658.8	44.4	933	7	CK270799	CK270799 EST716877
19	654	44.0	965	7	CK277059	CK277059 EST723177
20	652.4	43.9	879	6	CB893745	CB893745 EST646537
21	651.2	43.9	872	7	CK250566	CK250566 EST734203
22	649	43.7	1011	7	CK162737	CK162737 FGAS01533
23	648.8	43.7	732	6	CA798979	CA798979 sat73d06.
24	645.6	43.5	954	7	CK269124	CK269124 EST715202

25	645	43.4	922	6	CB981331	CB981331 CAB70004-
26	644.6	43.4	777	6	CA801356	CA801356 sau04f04.
27	641.8	43.2	902	7	CK279131	CK279131 EST752509
28	641.8	43.2	932	7	CK262812	CK262812 EST708890
29	641.8	43.2	945	7	CK270303	CK270303 EST716381
30	639	43.0	926	7	CF355380	CF355380 V-B-127E0
31	638	43.0	866	7	COI15240	COI15240 GR_E5016
32	637	42.9	948	7	CK276995	CK276995 EST723073
33	636	42.8	918	7	CK272097	CK272097 EST718175
34	635.4	42.8	983	7	CK262945	CK262945 EST709023
35	631	42.5	958	5	BQ165469	BQ165469 EST611338
36	627.8	42.3	959	7	CK261083	CK261083 EST707161
37	626.2	42.2	637	4	BI942096	BI942096 sfl6a09.X
38	626	42.2	937	7	CK277371	CK277371 EST723449
39	625.8	42.1	632	6	CA851546	CA851546 D14H08 P0
40	625.8	42.1	966	7	CK274663	CK274663 EST720741
41	625.4	42.1	859	7	CK274295	CK274295 EST720373
42	625.4	42.1	955	7	CK274554	CK274554 EST720632
43	625.2	42.1	859	7	CF214876	CF214876 CAST0001
44	625.2	42.1	942	7	CK277159	CK277159 EST723237
45	623.2	42.0	793	7	CF921046	CF921046 gmrhRw3-

## ALIGNMENTS

RESULT 1  
LOCUS CL970400 1191 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC041243 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL970400  
VERSION CL970400.1 GI:52395409  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
REFERENCE 1 (bases 1 to 1191)  
AUTHORS Ma, L., Wang, C., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.  
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
JOURNAL Unpublished (2004)  
COMMENT Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80486676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers  
source  
1. .1191  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Express Library"  
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN  
Query Match 55.2%; Score 819.6; DB 9; Length 1191;  
Best Local Similarity 81.0%; Pred. No. 5.3e-220;  
Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
QY 80 GAGACATTCCTATTACCTCAGTCAAGTCAAGGACACCTCGACAGCTCTGCGAC 139  
DB 13 GATACCTTCCTCTTACCTCGAGTCTGTGAACAGAGGCCACCTCGACAGCTCTGCGAC 72  
QY 140 CAAATCTCCGATGTGTCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199









Db 585 GACTTCAGGCCCCGGGATGATCAGCATCAACCTCGACCTGAAGAAGGGCGG---CAACAGG 529

Qy 1160 TTCTTGAAGACTCTCTGATATGACACATTCGGCAGAGAGGACCTGACTTCAATCGGAA 1219

Db 528 TTTCATCAGACCGCCGATACGACCTTTGGCCGTGACGACCGCCGACTTCACTGGGAG 469

Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCGCTAAGGCCATTCAATCCACTGCAATGTGCTG 1279

Db 468 GTGGTCAAGCCCTCAAGAGGATCCGCTTGAAGATGATTGGGAAGTTCACTGGACAT 409

Qy 1280 GGAGTTTTTTAGCGT 1294

Db 408 GAGTTTCATCTTCGT 394

RESULT 5

CK606439 740 bp mRNA linear EST 22-JAN-2004

LOCUS gmhrw6-12\_D09\_T7 Soybean root hair subtracted cDNA library

DEFINITION gmhrw6 Glycine max cDNA, mRNA sequence.

ACCESSION CK606439

VERSION CK606439.1 GI:41146228

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 740)

REFERENCE Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

AUTHORS Expressed sequence tags from soybean root hair subtractive cDNA library

JOURNAL Unpublished (2003)

COMMENT Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-4752

Fax: 573-882-0588

Email: stacey@missouri.edu

Single pass sequence

Seq primer: T7.

FEATURES

source

Location/Qualifiers

1..740

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/tissue\_type="root hairs"

/clone\_lib="Soybean root hair subtracted cDNA library

gmhrw6"

/note="Organ: root hairs; Vector: pCEM-T-Easy; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 6 hours."

ORIGIN

Query Match 49.6%; Score 736.8; DB 7; Length 740;

Best Local Similarity 99.7%; Pred. No. 1.2e-196;

Matches 738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 746 CTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGGTTTGTCTCATTTGAGGTCT 805

Db 1 CTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGGTTTGTCTCATTTGAGGTCT 60

Qy 806 CACGGTGATGCTGCTCTACCGGCCCAAGATCATCATGACTTACGGAGATGGGT 865

Db 61 CACGGTGATGCTGCTCTACCGGCCCAAGATCATCATGACTTACGGAGATGGGT 120

Qy 866 GCTCATGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGTGCT 925

Db 121 GCTCATGGTGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGTGCT 180

Qy 926 TACATTGTGAGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGGTGCATT 985

Db 181 TACATTGTGAGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGGTGCATT 240

Qy 986 GTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTTGTCTGTCTTTGTTCACACCTAT 1045

Db 241 GTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTTGTCTGTCTTTGTTCACACCTAT 300

Qy 1046 GGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAATTTGATTTTC 1105

Db 301 GGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAATTTGATTTTC 360

Qy 1106 AGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTG 1165

Db 361 AGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTG 420

Qy 1166 AAGACTGTGTCATATGGACACTTCGCGAGAGAGGCCCTTGACTTCACATGGGAAGTGGTC 1225

Db 421 AAGACTGTGTCATATGGACACTTCGCGAGAGAGGCCCTTGACTTCACATGGGAAGTGGTC 480

Qy 1226 AAGCCCCCTCAAGTGGGAGAAGGCCCTAAGGCCATTCAATCCACTGCAATGTGCTGGAGTT 1285

Db 481 AAGCCCCCTCAAGTGGGAGAAGGCCCTAAGGCCATTCAATCCACTGCAATGTGCTGGAGTT 540

Qy 1286 TTTTAGCGTTGCCCTTATAATGCTATTATTCATTAATCCATTAATCCACTGCTCTGTGT 1345

Db 541 TTTTAGCGTTGCCCTTATAATGCTATTATTCATTAATCCATTAATCCACTGCTCTGTGT 600

Qy 1346 TTTTCTCTCGTCTGCT 1405

Db 601 TTTTCTCTCGTCTGCT 660

Qy 1406 ATGATCAACAATAAATAATGACTCTCTGTTTTCGACCAATGTTGTCTCTCTCTCTCTCTCT 1465

Db 661 ATGATCAACAATAAATAATGACTCTCTGTTTTCGACCAATGTTGTCTCTCTCTCTCTCTCT 720

Qy 1466 CAAAAGAAGTGTCCAAGTT 1485

Db 721 CAAAAGAAGTGTCCAAGTT 740

RESULT 6

B1968543/c 775 bp mRNA linear EST 23-OCT-2001

LOCUS GM830005B12E10 Gm-r1083 Glycine max cDNA clone Gm-r1083-1771 3',

DEFINITION mRNA sequence.

ACCESSION B1968543

VERSION B1968543.1 GI:16342948

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 775)

AUTHORS Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Corvett,V., Expelting,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.

TITLE A Functional Genomics Program for Soybean (NSF 9872565)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: AW132830 corresponding to Gm-cl013-3165 (5')  
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)  
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics

University of Illinois

Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA

Tel: (217) 244-6147

Fax: (217) 333-4582

Email: l-vodkin@uiuc.edu

This clone is available through: Incyte Genomics, 4633 World Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: <http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio>















KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL

REFERENCE  
AUTHORS

JOURNAL

COMMENT

Unpublished  
2 (bases 1 to 1498)  
Genoscope.  
Direct Submission  
Submitted (18-Nov-2003) Genoscope - Centre National de Sequencage :  
BP 131 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_BF/Full  
length  
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.  
Location/Qualifiers  
1..1498  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3702"  
/clone="GSLTSL602H07"  
/tissue\_type="adult vegetative tissue"  
/plasmid="PCWSPORT 6"  
/complement(1..1498)  
/gene="At3g17390"

FEATURES  
source

Query Match 46.5%; Score 690.4; DB 3; Length 1498;  
Best Local Similarity 75.3%; Pred. No. 2e-183;  
Matches 892; Conservative 0; Mismatches 281; Indels 3; Gaps 3;

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 139  
DB 72 GAATCTTTTGTTCACATCTGNATCCGTCAAGGAGGACATCCCGAAGCTTTGTGAT 131

QY 140 CAAATCTCCGATGCTCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGCG 199  
DB 132 CAGATCTCCGACGCTATCTCGATGCTTGCCTTGAACAGACCCCTGAGAGCAAGTTGCT 191

QY 200 TCGGAACATGACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCAACCAAGGCC 259  
DB 192 TGTGAGACTTGTACCAAGACTAACATGGTTCATGGTCTTGTGAGAAATCAACCAAGGCT 251

QY 260 AAGTTGACTACGAGAGATCGTGCCTGACCTGACCTGAGGAAACATCGGCTTCGTCTCAAA 319  
DB 252 AAGTTGATACGAGCAGATTGTTCTGTAACATGCGGTGAGATTGGATTCTGCTCTGCT 311

QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGGCTCTTGTAAACATTGAGCAGCAGGCCCT 379  
DB 312 GAGCTTGGTCTAGATGCTGACAAATTCGAGGTTCTGTTAAACATTGAGCAACAGAGTCT 371

QY 380 GATATTGCCAGGCTGTGACGGCCACCTTACCAAGACCCGAGGAAATCGGTGTGGA 439  
DB 372 GACATTGCAAGGTTTTCATGTCATCTCACTAAGAACCCAGAGGAGGTTGGAGCTGCT 431

QY 440 GACCAGGGTCACATGTTTGGCTATGTCACGAGCGAAACCCAGAAATTGATGCCATTGAGT 499  
DB 432 GACCAAGGTCACATGTTTGGGTATGCTACTGATGAGACTCCTGAGCTCATGCTCTTACT 491

QY 500 CATGTTCTTGCAACTAACTCGTGTCTCACCAGAGTTGCGAAGAACGAACTGCTGC 559  
DB 492 CAGGTTCTCGCTACTAAGCTTGGAGCTAAACTCACTGAAGTTTGGCAAGAAATGGAATTCG 551

QY 560 CATGTTTCCAGCCCTGATGGGAAACCCCAAGTGACTTGTGAGTATTACAAATGACAAACG 619  
DB 552 CTTGTTGAGGCCAGATGTTAAGACTCAAGTCACTATTGAGTACATCAACGAAACGGA 611

QY 620 GCCATGGTTTCCAGTTTCCGTGTCACACTGTGTCTTATCTCCACCCCAACATGATGAGACTGTG 679  
DB 612 GCCATGGTTTCCGTGAGTGTCCACACTGTCTCATCTCAACACAGCATGACGAGACTGTG 671

QY 680 ACCAAGCAGAAATGTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG 739  
DB 672 ACTAAGCATACATCCACCTCATCTTCAACCACTCTCATCAACCCAGTATCCAGAC 731

QY 740 AAGTACCTTGTGAGAGAACCAATTTTCCACTTTGAACCCCTCTGGCCGTTTGTGTCATGGA 799  
DB 732 AATACCTTGTGAGAAACCACTTCCATCTCAACCCATCTGGTCTGTTTGTATCCGA 791

QY 800 GGTCTCTCAGCGTGTGCTGCTCACCGCCGCAAGATCATCATCGATACATTCACGAGGA 859  
DB 792 CGTCTCTCATTTTATTCTTTTCTTACTGCGTAAATCAAGATGGATACTTATTATTTT 851

QY 860 TGGGTGTCATGTTGGTGGTCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919  
DB 852 TGTTTTTCACA-CTTATTGTGCTTCTCTGTAAATGACCCAAACCAAGGTTGACATTAT 910

QY 920 GGTGCTTACATGTGAGACAGGCTCTAAGAGCATTTGTGGCAAGTGAGTACGACGAAG 979  
DB 911 GGGGCTTACATCTTTATTCAAGCAGCTAATATCATTTGAGCCAGTTGGTAGCGGCGG 970

QY 980 TGCATTGTCAAGTCTTATGCCATTGGTGTGCCCGAGCCCTTTGTCTGCTCTTTGT-TGA 1038  
DB 971 GTCAATTGTTCAAGTCTCGTATGCCATTTTTCCTGAGCCATTGTCGTGTTTCTGTGTA 1030

QY 1039 CACCTATGCGACCGGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGAGACTT 1098  
DB 1031 CAGTTATGGAACAGGAAAGATACCAAGCAAGGAGATTCTTGAGATTGTGAAGGAGATT 1090

QY 1099 TGATT-TCAGGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGTGGGATAACA 1157  
DB 1091 TGATTCTCAGGCCAGGTATGATCTCCATTAACCTTGATCTGAAGAGAGGAGGTAATGTTA 1150

QY 1158 GGTCTTCAAGACTGCTCATATGACACTTCCGGCAGAGAGACCTTGACTTTCACATGGG 1217  
DB 1151 GGTCTTCAAGACTGCTGCTATGCTACTTTGGAAGGAGCAGTGTGATTTCACTCTGG 1210

QY 1218 AAGTGGTCAAGCCCTCAAGTGGGAGAAGGCTAAG 1253  
DB 1211 AGGTAGTCAAGCCACTCAAGTCTAAGTCTAACAAGGTCCAAG 1246

RESULT 13  
CB330707  
LOCUS  
DEFINITION  
CB330707  
VERSION  
CB330707.1  
GI:28879836  
EST.  
Ipomoea batatas (sweet potato)  
Ipomoea batatas  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.  
Jankowicz.J., Berenyi,M. and Burg,K.

TITLE Identification of adaptation specific differences in the mRNA  
expression profile of drought tolerant and sensitive sweetpotato  
Unpublished (2004)  
JOURNAL  
COMMENT Contact: Berenyi M.  
Department of Biotechnology  
ARC Seibersdorf Research GesmbH  
A2444 Seibersdorf, Austria  
Tel: +43 50550 3524  
Fax: +43 50550 3444  
Email: Maria.Berenyi@arcs.ac.at  
PCR Primers  
FORWARD: lambda Triplex 5' Screening Amplimer  
BACKWARD: lambda Triplex 3' Screening Amplimer  
Insert Length: 1235 Std Error: 0.00  
Seq primer: lambda Triplex Sequencing Primers  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
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/clone\_lib="Sweetpotato cDNA library"  
/note="Vector: Triplex2; Site 1: Sfi A; Site 2: Sfi B;  
Ipomoea batata (Lam) L.; Smart cDNA library Construction  
Kit; Clontech: PT3000-1"

ORIGIN  
Query Match 46.1%; Score 685; DB 6; Length 1235;  
Best Local Similarity 83.4%; Pred. No. 6.4e-182;  
Matches 778; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 321 ATGTGGACTTGATGCTGACAACTGCAAGTCTTGTAACATTTGAGCAGCAGAGCCCTG 380  
Db 1 ATGTTGGTTGGATGCTGACAACTGCAAGTCTTGTTAACTTTGAGCAGCAGAGTCCTG 60

QY 381 ATATTGCCAGGGTGTGACGGCCACCTTACCAAGAGCCCGAGNAATCGTGTCTGGAG 440  
Db 61 ATATTGCCAGGGTGTGACGGTGTCTTACCAAGAGAGCTGAGGATATTTGTTGCTGGT 120

QY 441 ACCAGGGTCACTGTTTGCTGATGCCAGGAGCAACCCAGAACTTGATGCCATTTGAGTC 500  
Db 121 ACCAGGGCCACATGTTTGATATGCCAGCAGACCCCTGAAATTGATGCCCTCAGCC 180

QY 501 ATGTTCTTGCACATAAATCGGTGTCTGCTCACCGAGTTTCGCAAGAACGGAACTCGCC 560  
Db 181 ATGTCCTTGCACCAAGCTTGGAGTGTGCTCACCAGGTCGGAAGGATGGGACCTGCG 240

QY 561 CATGTTGAGGGCTGATGGGAACCCCAAGTCACTGTTGAGTATTACATGACACAGGTG 620  
Db 241 CTTGGCTCAGACTGATGTGTAACCTCAGGTCACTGTTGAGTACTACATGACATGGTG 300

QY 621 CCATGTTCCAGTTCGTGTGCACACTGTGCTTATCTCCACCCAAACATGATGAGCTGTGA 680  
Db 301 CCATGTTCTGTCCGCTGACACACTGTTCTGATCTCTACTCAGCAGCAGAGACTGTCA 360

QY 681 CCAACGACGAATTCGAGCTGACCTCAAGGACATGTGATCAAGCCGGTGTATCCCGAGA 740  
Db 361 CCAATGATGAATTCGCTCGTGATCTCAAGGACATGTCTCAAGCCTGTGATTCCTCGAGA 420

QY 741 AGTACCTTATGAGAGACATTTTCCACTTGAACCCCTCTGGCCGTTTGTTCATTGGAG 800  
Db 421 AGTACCTTATGAGAGACATCTTTACCTCAACCCATCAGGCCGATTTGTTCATTGGTG 480

QY 801 GTCTCTCAGCGTGTGCTGTCTCACCGCCGGAAGATCATCATCATCTTACCGAGGAT 860  
Db 481 GACCTCATGTTGCTGTGGCTTCACTGGCCGCAAGATCATTTATGACATACGTTGAT 540

QY 861 GGGGTGCTCATGGTGGTGTCTTTCTCCGGAAGGATCCCAACCAAGGTTGATAGAGTG 920  
Db 541 GGGGTGCTCACGAGGAGGTGCTTTCTCTCGGGAAGACCCCTACCAAGGTGGACAGAGTG 600

QY 921 GTGCTTCAATTTGTGAGACAGGCTGCTAAGACATTTGGCGAAGTGGACTAGCAGAAGGT 980  
Db 601 GAGCTATGTGTGAGGCAAGCTGCCAAGACATTTGTTCCAAAGGGCTTGTCTCGTAGGT 660

QY 981 GCATTTGTGCAAGTGTCTTATGCCATTTGGTGTGCGCGAGCCCTTGTCTCTTTGTTGACA 1040  
Db 661 GCATTTGTGAGGTGTCTATCGCCATTTGGTGTGCTGCAACCATTTGTCCGTCTTCGTAGATA 720

QY 1041 CCTATGGCACCGGAAGATCCATATAGGAGATTTCTCAACATTTGTGAGGAGACCTTTG 1100  
Db 721 CCTATGGAAACCGGAAGATTTCCGACCAAGGAATCTCTCAAGATTTGTGAAGAGACATTTG 780

QY 1101 ATTTTCAGCCCGGTATGATCTTCCATCAACCTTGTATCTCAAGAGGGTGGGATACACAGT 1160  
Db 781 ATTTTCAGCCCTGTTATGATCGCCATCAACCTTGGACCTCAAGAGGGTGGCAACACAGGT 840

QY 1161 TCTTGAAGACTGTGTCATATGACACTTTCGCGACAGAGGACCTGACATTCATCGGGAAG 1220  
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## RESULT 14

CK269428  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CK269428 1008 bp mRNA linear EST 03-AUG-2004  
EST715506 potato abiotic stress cDNA library Solanum tuberosum CDNA  
clone POACM76 5' end, mRNA sequence.  
CK269428  
CK269428.1 GI:39826406  
EST.  
Solanum tuberosum (potato)  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 1008)  
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.  
Generation of ESTs from abiotic stressed potato tissue  
Unpublished (2003)  
Other ESTs: EST715507  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.  
Seq primer: ATT TAG GTG ACA CTA TAG.

## FEATURES

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supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 45.4%; Score 673.6; DB 7; Length 1008;  
Best Local Similarity 83.8%; Pred. No. 1e-178;  
Matches 774; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

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QY 86 GAAACTTCTATTACCTCTGAGTCTGTGAACGAGGTCACCCAGACAGCTCTGTGAT 145  
DB |||||  
QY 140 CAAATCTCGAGTCTGTCTCTCGACGCTTGCTTTGAACAGGACCCAGACAGGTTGCC 199  
DB |||||  
QY 146 CAGATCTCTGATCGAGTCTTGATGCTGCTTGAGCAGATCTCGAGCAGAAAGTTGA 205  
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QY 200 TGGAAACATGACACCAAGACCAACTTGGTCATGCTTTCGAGAGATCACCAAGGCC 259  
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QY 260 AAGTTGACTACGAGAGATCGTGGTGACCTGCAGGACATCGGCTTCGCTCAAC 319  
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QY 380 GATATTTGCCAGGGTGTGACGGCCACTTTACCAAGACCCGAGAAATCGGTGTGGA 439  
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QY 386 GATATTTGCTCAAGGTGTCCATGTCCTGACCAACGCGCGAGGAGATGGTGTGCTGT 445  
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RESULT 15

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EST720123 potato abiotic stress cDNA library Solanum tuberosum cDNA  
clone POAD591 5' end, mRNA sequence.  
CK274045  
CK274045.1 GI:39831023  
EST.  
Solanum tuberosum (potato)  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 979)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  
Generation of ESTs from abiotic stressed potato tissue  
Unpublished (2003)  
Other ESTs: EST720124  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@igr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: AAT TAG GTG ACA CTA TAG.  
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/note="Vector: pCMVsp6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d. Set 4 were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cDNA library. RNA sample."

FEATURES

source  
Query Match 45.1%; Score 669.6; DB 7; Length 979;  
Best Local Similarity 81.6%; Pred. No. 1.3e-177;  
Matches 774; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

ORIGIN

61 TTAAAGTATTAGATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACA 120  
QY



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2	1064.4	71.7	1659	8	AB0623358	Phascolus	
3	912.4	61.4	1173	8	AY560003	Medicago	
4	866.8	58.4	1479	6	AR439798	Sequence	
5	866.8	58.4	1479	8	LEGALMSGA		
6	866.8	58.4	1526	8	BT012699	Lycopersi	
7	864.8	58.2	1637	8	AF346306	Blaeagnus	
8	858.8	57.8	1667	8	LEGALMSGB		
9	854	57.5	1437	8	POPSAMPDPT		
10	852.8	57.4	1303	8	AB041534	Camellia	
11	852.4	57.4	1523	8	AY635050	Solarium b	
12	850.4	57.3	1776	8	CS1277206	Camellia	
13	849.8	57.2	7894	8	AP004964	Lotus cor	
14	848.6	57.1	1381	8	CRSAMS2		
15	847.6	57.1	1628	8	MCU79767	Mesembryant	
16	847.4	57.1	1886	8	AF531479	Carica pap	
17	845.2	56.9	1531	8	AF321001	Suaeda ma	
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RESULT 2  
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complete cds.  
ACCESSION AB062358  
VERSION AB062358.1 GI:18157330  
KEYWORDS  
SOURCE Phaseolus lunatus (lima bean)  
ORGANISM Phaseolus lunatus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Phaseolus.  
REFERENCE 1  
AUTHORS Arimura, G., Ozawa, R., Nishioka, T., Boland, W., Koch, T., Kuhnemann, F.  
and Takabayashi, J.  
TITLE Herbivore-induced volatiles induce the emission of ethylene in  
neighboring lima bean plants  
JOURNAL Plant J. 29 (1), 87-98 (2002)  
MEDLINE 22056020  
PubMed 12060229  
REFERENCE 2 (bases 1 to 1659)  
AUTHORS Arimura, G., Takabayashi, J. and Nishioka, T.  
TITLE Direct Submision  
JOURNAL Submitted (25-MAY-2001) Gen-ichiro Arimura, Kyoto University,  
Laboratory of Insect Physiology, Graduate School of Agriculture,  
Kitashirakawa Oiwake-cho, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
(E-mail: arimuragokais.kyoto-u.ac.jp, Tel:81-75-753-6308,  
Fax:81-75-753-6312)

FEATURES  
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ORIGIN

Query Match 71.7%; Score 1064.4; DB 8; Length 1659;  
Best Local Similarity 89.8%; Pred. No. 1.2e-268;  
Matches 1165; Conservative 0; Mismatches 131; Indels 2; Gaps 2;  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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ORGANISM  
AY560003  
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AY560003.1 GI:48093936  
Medicago sativa  
Medicago sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE  
AUTHORS  
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Query Match 61.4%; Score 912.4; DB 8; Length 1173;  
Best Local Similarity 86.2%; Pred. No. 1.1e-228;  
Matches 1009; Conservative 0; Mismatches 161; Indels 0; Gaps 0;  
Qy 80 GAGACATTCCTATTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGCGAC 139  
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Qy 140 CAATCTCCGATGCTGCTCGAGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
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Qy 260 AACGTTGATGAGAGAGATCGTGGTGACACCTGCGAGAACATCGGCTTGTCTCAAAC 319





Qy	900	CCACCAAGGTTGTATAGAGTGGTGCTTACATTGTGTGACACAGCGCTGTAAAGACATTTGTGG	959
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Qy	960	CAAGTGACATAGCCACAGAAAGGTGCATTCTGCAAGTGTCTTATGCCATTGGTGTGCCCGAGC	1019
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Db	1123	AGATCGTTAAGGAGAACTTTTGACTTTCAGACCTTGGAAATGATGTCCATTAACTTGGATTTGA	1182
Qy	1140	AGAGGGGTGGGAATTAACAGGTTCCTTGAAGACTGCTGCATATGGACACTTCGGCGCAGAGAGG	1199
Db	1183	AGAGGGGTGGCAATAGAAGATTCCTTGAANAACCTGCTGCTATGGTCACTTTGGACGTGATG	1242
Qy	1200	ACCTTGACTTTCACATGGGAAAGTGGTCAAGGCCCTTCAAGTGGGAGAGGCCCTTAAGGGCCATT	1259
Db	1243	ACCCCGATTTTCACATGGGAAGTTGTCAAGCCCCCTCAAGTGGGAAAGGCCCCACAGACTAAT	1302
Qy	1260	CATTCCACTGCAATGTCTCGGAGTTTTTTT	1289
Db	1303	AAGTGTCTTGCTATGTTTGTGTTCTTTGTT	1332

## RESULT 5

LESALMSGA	LESALMSGA	1479 bp	linear	PLN 12-MAY-1995
LOCUS	L. esculentum S-adenosyl-L-methionine synthetase mRNA, complete CDS.			
DEFINITION				
ACCESSION	Z24741			
VERSION	Z24741.1	GI:429103		
KEYWORDS	S-adenosyl-L-methionine synthetase.			
SOURCE	Lycopersicon esculentum (tomato)			
ORGANISM	Lycopersicon esculentum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 1479)			
AUTHORS	Espartero J., Pintor-Toro, J.A. and Pardo,J.M.			
TITLE	Differential accumulation of S-adenosylmethionine synthetase transcripts in response to salt stress			
JOURNAL	Plant Mol. Biol. 25 (2), 217-227 (1994)			

CDs

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Qy	120	ACCCTGACAAGCTCTCGCACCACAAATCTCCGATGCTGTCTCGACGGCTTCGCTTGAACAGG	179	
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Qy	180	ACCAGACAGCAAGGTGCTCGAAACATGACCAAGACCAACTTGGTTCATGGTCTTCG	239	
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Qy	240	GAGAGATCACCAACCAAGGCCACGTGTGACTACGAGNAGATCGTGGTGGACACCTGCAGGA	299	
Db	283	GTGAGATCAACAACCAAGGCTATTGTAGACTATGAGAAGATTGTGGTGGACACATGCGGTA	342	
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Db	343	ATAATTGGAATTGTTCTGATGATGTTGGTCTTGTGCTGACAACTGCAAGGTCCTTGT	402	
Qy	360	ACATTGAGCAGCAGAGCCCTGATATTGCCACGGGTGTGCACGGCCACCTTACCAAAAGAC	419	
Db	403	ACATTGAGCAGCAAGTCTCTGATATTGCTCAAGGTGTCCACGGCCATCTGACCAACGCC	462	
Qy	420	CCGAGAAATCCGGTGTGAGACCAAGGGTCAATGTTTGGCTATGCGCAGGACGAAACCC	479	
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Qy	480	CAGATTGATGTCATGTAGTCATGTTCTTGCAACTTAACTCGGTGCTCGTCTCACCGAGG	539	
Db	523	CTGAATTAATGCTCTCAGTCAAGTGTGCAACTTAACTTGGTGCCCGTCTTACAGAAG	582	
Qy	540	TTTCGCAAGAACCGAACCTGCCCATGGTTGAGGCTCTGATGGGAAAAACCAAGTGACTGTG	599	
Db	583	TCGCAAGNATGGCACTTGGCTGGTGGAGGCTGATGGCAAGACCCNAGTTACTGTG	642	
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Qy	660	CCCAACATGATGAGACTGTGACCAACGAGGAAATTTGCAGCTGACCTCAAGGAGCATGGA	719	
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Qy	720	TCAACGCGGTGATCCCGGAGAGTAGTACCTTTGATGAGAAGACCAATTTTCCACTTGAACCCCT	779	
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Qy	780	CTGGCCGTTTGTTCATTTGAGGTCCTCAGGCTGATGCTGGTCTCACCGCGCGCAAGATCA	839	
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Qy	840	TCATCGATATTTACGAGAGATGGGTGCTCATGGTGGTGGTGGTCTTTCCTCGGGGAAGGATC	899	
Db	883	TCATCGACACTTATGGTGGTGGGTGCTCATGGTGGTGGTGGTCTTTCCTCGGGCAAGACC	942	

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QY 1260 CATTCACACTGCAATGCTGCGGAGTTTTTT 1289
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LOCUS Lycopersicon esculentum clone 113572R, mRNA sequence.
DEFINITION BT012699
ACCESSION BT012699
VERSION BT012699.1 GI:47104114
KEYWORDS FLI CDNA.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 1526)
AUTHORS Kirkness, E.F., Wang, W. and Vazeille, A.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA
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ORIGIN
Query Match 58.4%; Score 866.8; DB 8; Length 1526;
Best Local Similarity 81.5%; Pred. No. 1.2e-216;
Matches 1003; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

QY 60 TTTAAGATTAAAGATGGCAGAGACATTCCTATTTACCTCAGATCAGTGAACGAGGGAC 119
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DEFINITION mRNA, complete cds.  
ACCESSION AF346306  
VERSION AF346306.1 GI:13540317  
KEYWORDS Elaeagnus umbellata  
SOURCE Elaeagnus umbellata  
ORGANISM Elaeagnus umbellata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
REFERENCE  
AUTHORS Lee, S.H. and An, C.S.  
TITLE S-adenosyl-L-methionine synthetase from two cDNA clones encoding  
Structures and expression patterns of the root nodule of  
Elaeagnus umbellata  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Lee, S.H. and An, C.S.  
TITLE Direct Submission  
JOURNAL Submitted (06-FEB-2001) School of Biological Sciences, Seoul  
National University, Seoul 151-742, Korea  
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DB 1253 ATTGTGAAGCCCTCAATGGGAGAGGCTCAATCTTAAGCAAGATCAGTCTGCTGCTG 1312  
QY 1280 GGAGTTTTTACGTTGGCCCTTAAATGCTTATTAATCAATACTTTCCAGCTGCTTGTGCT 1339  
DB 1313 CTGCTCTGAGTGTGCTTTATTTGTGGTACTTTATTAATTAATTTTCTGTTTATTTGCT 1372  
RESULT 8  
LESALMSGB  
LOCUS L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete CDS.  
DEFINITION S-adenosyl-L-methionine synthetase.  
ACCESSION Z24742  
VERSION Z24742.1 GI:429105  
KEYWORDS S-adenosyl-L-methionine synthetase.  
SOURCE Lycopersicon esculentum (tomato)

ORGANISM	Lycopersicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 1667)
AUTHORS	Espartero,J., Pintor-Toro,J.A. and Pardo,J.M.
TITLE	Differential accumulation of S-adenosylmethionine synthetase transcripts in response to salt stress
JOURNAL	Plant Mol. Biol. 25 (2), 217-227 (1994)
MEDLINE	94289646
PUBMED	8018871
REFERENCE	2 (bases 1 to 1667)
AUTHORS	Espartero,J. and Pardo,J.M.
TITLE	Differential expression of three S-adenosylmethionine synthetase genes in response to stress in tomato
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1667)
AUTHORS	Pardo,J.M.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1993) Jose M. Pardo, Instituto de Recursos Naturales y Agrobiologia., C.S.I.C., Avda. Reina Mercedes, Sevilla, Sevilla, 41080, Spain
FEATURES	Location/Qualifiers
source	1..1667
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	/dev_stage="seedling"
	295..1476
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CDS	
	57.8%; Score 858.8; DB 8; Length 1667;
	Best Local Similarity 83.2%; Pred. No. 1.5e-214;
	Matches 977; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
QY	80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 139
DB	298 GAGACTTTCTTATTCATCTGAATCAGTCAGTCAACGAGGGACATCCCGACAAAGCTCTGTGAC 357
QY	140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACGAGGCCACGACGAGGAGTTGCC 199
DB	358 CAGGCTCTGATGCGAGTGTGCTGCTGCTAGCTCAGGACCCCTGAAAGCAAGTTGCA 417
QY	200 TCGAAACATGACCAAGACCAACTTGGTCTTCGGAGAGATCACCAAGGCC 259
DB	418 TGTGACACTTGTACCAAGACCAACTTAGTTATGGTCTTGGAGAGATCACCAAGGCC 477
QY	260 AACGTTGACTACGAGAAGATCGTGGGTGACACCTCGAGGAACATCGGCTTGTCTCAAC 319
DB	478 AATATTGATTATGAGAAGATTGTACGTGACACTTGCCTGGGAAATTTGATTGTGCCCT 537
QY	320 GATGTGGGACTTGACTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGCAGGCCCT 379
DB	538 GATGTTGGTTGGATGCTGACAAATGTCAGAGTCCTTGTGAACATTGAGCAGCAGGCCCT 597
QY	380 GATATTGCCAGGGTGTGACGCGCCACCTTACCAAAAGACCCGAGGAATCGGTGCTGGA 439

## ORIGIN

Query Match 57.8%; Score 858.8; DB 8; Length 1667;  
 Best Local Similarity 83.2%; Pred. No. 1.5e-214;  
 Matches 977; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

## RESULT 9

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 LOCUS  
 DEFINITION  
 POPULUS x generosa tissue-type leaf S-adenosyl methionine synthetase mRNA, complete cds.  
 M73430  
 VERSION  
 M73430.1 GI:497899  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Populus balsamifera subsp. trichocarpa x Populus deltoides  
 Populus balsamifera subsp. trichocarpa x Populus deltoides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Malpighiales; Salicaceae; Populus.

598 GATATTGCTCAAGGTGTTTCATGTCATTTGACTAAGCGACCTGAGGAGATTGGTCTGGT 657  
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 658 GACCAGGGTCACATGTTTGGCTATGCCACTGACGAGACACCGGAGTTTATGCCCTTAGC 717  
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 560 CCATGTTTGAGGCTGATGGGAAACCCCAAGTGAATGTTGAGTATTCACATGACAAACGGT 619  
 778 TCTTGGCTTAGACCTGATGGTAAACACAAGTGAATGTTGAGTATTCACATGACAAATGGT 837  
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 838 GCTATGGTTCCTCTACGTTTTCACACTGTTTAAATCTCCACTCAGCATGATGAGACTGTT 897  
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 740 AAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGSCCGTCTTGTCTCATTTGA 799  
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 800 GGTCTCTACGGTGATGCTGCTCACCGGCCGCAAGATCATCATCGACTACTTACGGAGGA 859  
 1018 GGACCTCACGGTGATGCTGCTCACTGCGCGTAAGATCATCATTTGACACATTCACGGAGGT 1077  
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 920 GGTGCTTACATTTGTGAGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCCAAGAG 979  
 1138 GGAGCCTATATCGTGAGGCAAGCAGCTAAGAGCATTTGTGCTAAGCGTCTTGGCCAGAGG 1197  
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 1258 ACTTATGAACTGGGAAGATCCCTGCAAGAGATTCTCAACATTTGTGAGGAGAACTTT 1317  
 1100 GATTTGAGGCCGCTGATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
 1318 GATTTGAGGCCGCGGAATGATTTCCATTAACTCGATCTACTGAGGGGTGGCAATGGTGA 1377  
 1160 TTCTTGAAGACTGCTGCATATGGACACTTGGCAGAGAGGCCCTTGACTTCAATGGGAA 1219  
 1378 TTCTTGAAGACTGCTGCTTATGGGCAATTTGGTAGAGATGATCTCTGACTTTCATCATGGGAA 1437  
 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCCCTAAG 1253  
 1438 GTAGTTAAGCTCTCAAGTGGGACCAAGCCTGAAG 1471

REFERENCE 1 (bases 1 to 1437)  
Van Doorselaere,J., Gielen,J., Van Montagu,M. and Inze,D.  
TITLE A cDNA encoding S-adenosyl-L-methionine synthetase from poplar  
JOURNAL Plant Physiol. 102 (4), 1365-1366 (1993)  
MEDLINE 94105359  
PUBMED 8278561

REFERENCE 2 (bases 1 to 1437)  
Van Montagu,M.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-1991) M. Van Montagu, Laboratorium voor Genetica,  
Universiteit Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium  
COMMENT On Jun 6, 1994 this sequence version replaced gi:169464.  
FEATURES  
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ORIGIN  
    Query Match 57.5%; Score 854; DB 8; Length 1437;  
    Best Local Similarity 83.0%; Pred. No. 2.8e-213;  
    Matches 974; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 72 AGATGCGAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACACCTTGACAAGC 131  
DB 58 AATGCGAGAGACTTTCCTATTACATCTGAATCAGTGAATGAGGACACCCAGATNAGC 117

QY 132 TCTGCGACCAATCTCCGATGTCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCA 191  
DB 118 TCTGTGACAGACTCTCTGATCGCTACTCGATGCTTGTGCGCAAGACCTTGACAGCA 177

QY 192 AGGTGCTCGGAAACATGCAACCAACCAACCTTGCTCATGTCTTCGAGAGATCACCA 251  
DB 178 AGGTGCGATCGGAGACTTGCATTAAGCAACCAACATGCTCATGTTTTCGCGAGATCACCA 237

QY 252 CCAAGGCCAACGTTGACTACGAGAAGATCGTGGTGACACACCTGCGAGAACATCGGCTTCG 311  
DB 238 CCAAGGCTGATGATGATTACGAGAGATTTGGGTGATCTATGCGAACAATGGATTCA 297

QY 312 TCTCAACGATGCGGACTTGATGCTGACAACCTGCAAGGTCTCTGTAAACATTTGAGCAGC 371  
DB 298 CATCTCGCATGCGGTCTTGATGCGGACAAATTTGCAAGGTCTCTAGTTAATTTGAGCAAC 357

QY 372 AGAGCCCTGATATTCGCGAGGTGTGCGAGGACCTTACCAAGACCCGAGGAATCG 431  
DB 358 AAGATCCTGATATTCGCGAGGTGTGCGAGGATCATGGTCAATTTCTCAAGAGACCCGAGGATTTG 417

QY 432 GTGCTGAGACACAGGTTCATGCTTTGGTGTATGCGACGAGCAAAACCCAGAAATTTGATGC 491  
DB 418 GTGCTGATGATCAGAGCCATATGTTTGGTGTATGCGCACTGACGAGACCCCTGATTTGATGC 477

QY 492 CATTTAGTCTATGTTCTTGAACATAAATCGGTGCTCGTCTCACCGAGGTTGCGAAGACG 551  
DB 478 CTTTGAAGCCAGCGTTTGGCTACCAAGCTTGGTGTGCTCGCTCACTGAGGTTGCTGAAGATG 537

QY 552 GAACCTGCCATGTTGAGGCTGATGGGAAACCAACCAAGTACTGTTGATGATTAATG 611  
DB 538 GAACCTTGGCATGTTGAGGCTGATGGGAAACCAACCAAGTACTGTTGATGATTAATG 597

QY 612 ACAACGGTCCCATGGTTCCAGTTCGTGTCCACACTGTGTCTTATCTCCACCCCAACATGATG 671  
DB 598 AATATGGAGCCATGGTTCTCTGCGCGTCCACACTGTTCTCATTTCTACTCAACATGATG 657

QY 672 AGACTGTGACCAACGAGAAATTCAGCTGACCTCAAGAGCATGTGATCAAGCCCGTGA 731  
DB 658 AGACTGTGACAAATGATGAGATTCGGGCTGATCTCAAGAGCATGTGATCAAGCCCGTGA 717

QY 732 TCCCGGAGAGTACCTTCGATGAGAGACCATTTTCCACTTGAACCCCTCTGGCCGCTTTG 791  
DB 718 TCCCTGAAAGTACTTGGATGAGAGACTATCTTCCATCTTAACCCCTCTTGGCCGCTTTG 777

QY 792 TCATTGGAGTCTCTCACGGTGTGCTGTGCTCACCGGCGCAAGATCATCATCGATCTT 851  
DB 778 TCATTGGTGTCTCTCATGCTGAGTCTGCTCTCACGGGAGCTAAGATTATTATTGACACTT 837

QY 852 ACGAGGATGGGGTGTCTATGCTGTGCTTCTTCCGGGAGGATCCCAACCAAGGTTG 911  
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QY 912 ATAGAGTGGTCTTACATTTGAGACAGGCTGTAAAGAGCATTTGGCAAGTGGACTAG 971  
DB 898 ATAGAGTGGAGCTTACATTTGAGCAAGCCGCAAGAGTATTGTTGCCAGTGGGCTTG 957

QY 972 CCAGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCGCGAGCCCTTTGTCTGTCT 1031  
DB 958 CTAGAGGTTGCATTGTTCAAGTCTCTATGCCATTGGCGTTCCTGAGCCCTCTGTCAAT 1017

QY 1032 TTGTTGACACTATGCGACCGGAGATCATGATGAAGAGATTTCTCAACATTTGGAAG 1091  
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QY 1092 AGAATCTTGAATTCAGGCGCGGTATGATCTCCATCAACCTTGCATCAAGAGGGTGGGA 1151  
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DB 1138 ATAGCAGGTTCTTGAAGACTGCTGAGCTTATGACACTTTTGGCAGAGATGACCCGACTTCA 1197

QY 1212 CATGGAGTGTGTCAGGCCCTTCAAGTGGAGAA 1245  
DB 1198 CATGGAGTGTGTCAGGCCCTTCAAGTGGAGAA 1231

RESULT 10  
AB041534  
LOCUS  
DEFINITION  
    Camellia sinensis SAM mRNA for s-adenosylmethionine synthetase,  
    complete cds.  
ACCESSION  
    AB041534  
VERSION  
    AB041534.1 GI:7594740  
KEYWORDS  
    s-adenosylmethionine synthetase.  
SOURCE  
    Camellia sinensis  
ORGANISM  
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
    asterids; Ericales; Theaceae; Camellia.  
REFERENCE  
    1 (bases 1 to 1303)  
AUTHORS  
    Feng, Y.F. and Liang, Y.R.  
TITLE  
    s-adenosylmethionine synthetase gene  
JOURNAL  
    Published Only in Database (2000)  
REFERENCE  
    2 (bases 1 to 1303)  
AUTHORS  
    Feng, Y.F. and Liang, Y.R.  
TITLE  
    Direct Submission  
JOURNAL  
    Submitted (09-APR-2000) Yan F. Feng, Tea Department Hua Jia Chi  
    Campus Zhe Jiang Uni., Tea Department; 268 Kai Xuan Road, Hang zhou  
    310029, China (E-mail:yf01@yahoo.com, Tel:81-5716971704,  
    Fax:81-5716971704)  
FEATURES  
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	S"			971		ACGTATGGGACTGGGAAGATTCCGACAAAGAGATTCTCAAGATTGTGAAAGAGAGCTTT		1039		
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	Best Local Similarity 82.8%; Pred. No. 5.6e-213;			1031		GATTTCAGGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATACAGG		1099		
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	11 GAGACTTTTCTATTACATCCGAATCTGTGAATGAGGGTCAACCCAGACAGCTCTGTGAT			1219		AGTGGTCAAGCCCTCAAGTGGGAGAGCCCTAAGGCCATTCATTCCAC 1267				
	140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTTGAACAGAGCCCAAGCAAGGTTGCC			1151		AGTGGTGAAGCCCTCAAGTGGGAGAGCCCTCAAGCTAATTTCTTNC CGC 1199				
	71 CAGATATCTGATGCGATTCTCGATGCGCTTGAACAGATCAAGACAGCAAGTTGCC			RESULT 11		AY635050		1523 bp		
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	131 TGTGAGACTTGCACCAAGACTTAACATGGTTCATGGTCTTCGGTGAATCAACCAAGGCC			DEFINITION		Solanum brevifolium S-adenosyl methionine synthase mRNA, complete		linear		
	260 AAGCTTGACTACGAGAGATCGTGGTGACACCTGACAGAAATCGGCTTCGTCTCAAC			ACCESSION		AY635050		cds		
	191 GCGGTAGACTATGAGAAGATTGCGGTGACACATCGCGCACCAATTTGTTCCGAT			VERSION		AY635050.1		GI:48928009		
	320 GATGTGGGACTTGTGACAACTGCAAGTTCCTTTGAACATTTGAGCAGAGAGCCCT			KEYWORDS		Solanum brevifolium		Solanum brevifolium		
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	380 GATATTGCCAGGTGTGCAGGCCACTTACCAAGACCCGAGGAAATCGGTCTCGA			ORGANISM		Solanum brevifolium		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	311 GATATTGCCAGGTGTGCACCGTCACTCTCACTAAGCGCCCGAGGAGATTGGTCCCGT			REFERENCE		1 (bases 1 to 1523)		asterids; lamids; Solanales; Solanaceae; Solanum.		
	440 GACAGGGTCACATGTTTGGCTATGCCAGGACGAAACCCAGAAATGATGCCATTGAGT			AUTHORS		Seo, H.W., Yi, J.Y., Moon, J.Y., Park, Y.E. and Cho, J.H.		SAM and polyamine levels in transgenic tomato fruits and potato		
	371 GACAGGGTCACATGTTTGGCTATGCCAGATGAACCTTCGAGCTGATGCCCTCAGC			TITLE		tuber with SAM synthase gene				
	500 CATGTTCTTGCAACTAACTCGGTGCTGCTCACCAGGTTTCGCAAGAACCGAACCTGC			JOURNAL		2 (bases 1 to 1523)		Unpublished		
	431 CATGTCCTTGCAACCAACTTGGTGGCCGCTTCACTGAAGTCGGAAGATGGAATCTTGC			REFERENCE		Seo, H.W., Yi, J.Y., Moon, J.Y., Park, Y.E. and Cho, J.H.				
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	491 CCTGTGTTAAGACCTGATGGCAAAACCCCAAGTGAATTTGATGATTTACATGAGAAGT			TITLE		Hoengke 3ri Doam Pyongchang, Gangwon 232 - 955, South Korea				
	620 GCCATGTTCCAGTTGCTGTCACACTGTCTTATCTCCACCAACATGATGAGACTGTG			JOURNAL		Location/Qualifiers				
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ORIGIN

Query Match 57.4%; Score 852.4; DB 8; Length 1523;  
Best Local Similarity 78.3%; Pred. No. 7.3e-213;  
Matches 1035; Conservative 0; Mismatches 286; Indels 1; Gaps 1;

QY	80	GAGACATTCCTATTTACCTCAGAGTCAGTGAACAGAGGACACCCCTCAGACGCTCTCGGAC	139
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QY	140	CAAAATCTCCGATGCTGTCTCGACGCTTGCTTTGAAACAGGACCCAGACGACGAGTTCGC	199
DB	172	CAGATCTCTGATGACGCTTCTTGATGCTGCTTTGAGCAAGATCCTGAGAGCAAGTTGCA	231
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DB	232	TGTGAACCTTGCAACCAAGACCACTTGGTCATGGTCTTTGGTGAGATCAACCAAGGCT	291
QY	260	AACGTTGACTACGAGAAAGATCGTGGCTGACACCTGCAGGAACATCGGCTTCGCTCAAC	319
DB	292	ATTGTAGACTATGAGAAATCGTGGTGACACATGCGGTAAACATTGGATTTGTTCTGAT	351
QY	320	GATGTGGGACTTGATGCTGACAACTGCAAGGCTCTTTGTAACATTTGAGCAGCAGCCCT	379
DB	352	GATGTTGGTCTTGATGCCGACAACTGCAAGGCTCTTTGTTTACATTGAGCAGCAAGTCT	411
QY	380	GATATTTGCCAGGCTGTGACGGCCACCTTACAAAGACCCGAGGAATCGTGTGGA	439
DB	412	GATATTTGCTCAAGGCTGACGGCCATCTGACAAACGCCCTGAGGAGATTGGTGTGT	471
QY	440	GACGAGGTACATGTTTGGCTATGCCACGAGCAACCCAGAACTTGATGCAATTTGAT	499
DB	472	GACGAGGTACATGTTTGGCTATGCCACGAGCAACCCAGAACTTGATGCAATTTGAT	531
QY	500	CATGTTCTTTCGCAACTAACTCGTGTCTCTCACCGAGGTTTCGCAAGAACGGAACCTGC	559
DB	532	CAGTGTCTTTCGCAACTAACTTGTGTGCGCCCTTACAGAACTTCGCAAGAAATGGCACTGC	591
QY	560	CAATGTTGAGGCTGATGGGAAACCCCAAGTGAATGTTGAGTATTAATGACAAAGCT	619
DB	592	CGTGTGTTGAAGCTGATGGCAAACTCAAGTTACTGTTGAGTACTGCAATGACATGCT	651
QY	620	GCATGTTTCCAGTTCGTTGTCACACTGCTTATCTCCACCCCAACATGATGAGCTGT	679
DB	652	GCAATGTTCCAAATTAGGGTTCACACTGTTCTCATCTCCACTCAACACGATGAGCTGT	711
QY	680	ACCAACGAGAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG	739
DB	712	ACAAATGATGAGATTGCGCGGACCTTAAGGAGCATGCTATCAAGCCAGTCAATCCAGAG	771
QY	740	AAGTACCTTGATGAGAAACCAATTTTCCATTGAACCCCTCTGGCGGCTTTGTCATGGA	799
DB	772	AAGTACCTTGACGAGAAACAATCTTCCACCTTAACCCATCTGGCGGATTTGTTATGCT	831
QY	800	GGTCTCACGGTGTGCTGCTCACGGCCGACAGATCATCATGATATTTACGAGGA	859
DB	832	GGACCTCATGGTGTGCTGCTCATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	891
QY	860	TGGGCTCATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	919
DB	892	TGGGCTCATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	951
QY	920	GCTGCTTACATTTGTGAGACAGGCTGTGAAGCATTTGTGGCAAGTGAATGACGAGG	979
DB	952	GCTGCTTACATTTGTGAGAGGCTGTGAAGCATTTGTGAGTGTGAGTGTGCTGCTGCTGCT	1011
QY	980	TGATGTCAGAGTGTCTTATGCCATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1039
DB	1012	TGATGTCAGAGTGTCTTATGCCATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1071

QY	1040	ACCTATGGCACCGGAAGATCATGATAGGAGATCTCAACATTTGTGAAGGAGAACTTT	1099
DB	1072	ACCTATGGCACCTGGAAGATCCCCGACAGGGAATTTTGAAGATCGTTAAGGAGAACTTC	1131
QY	1100	GATTTGAGGCGGCTATGATCTCCATCAACCTTTGATCTCAAGAGGGTGGGAATAACAGG	1159
DB	1132	GACTTCAGACCTGGAATGATGCTCAATTAACCTTTGATTTGAAGAGGGTGGCAATGGAGA	1191
QY	1160	TTCTTTGAAGACTGCTGCATATGACACATTTCCGACAGAGAGCCCTGACCTTCACATGGAA	1219
DB	1192	TTCTTTGAAGACTGCTGCCTATGCTCATTTTGGACGTCGACGCTGATTTTCAATGGAA	1251
QY	1220	GTGGTCAAGCCCTCAAGTGGGAGAGCCCTAAGCCATTTCATCCACTGCAATGTGCTG	1279
DB	1252	GTGTCAGAGCCCTCAAGTGGGAAACCCCAAGACTAATAAGTGTCTGAAAGTGTCTGC	1311
QY	1280	GGAGTTTTTTAGCGTTGCGCTTATATGCTATATTCATATCCATACTTTCCAGCTCCCTGT	1339
DB	1312	CTATGTTTTTTTCTCTTTGTTGCTTGTGGCTTTTGAATCCCTGTGTTGCTGT	1371
QY	1340	CTGTGT-TTTTCTCTCGTCCTCTCTCTATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT	1398
DB	1372	CTATGATTTTCTCTTTTGTGACCTTTTGTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCT	1431
QY	1399	TT 1400	
DB	1432	TT 1433	

RESULT 12  
CS1277206 1776 bp DNA linear PLN 28-MAR-2000  
LOCUS  
DEFINITION  
Camellia sinensis gene for s-adenosylmethionine synthetase.  
ACCESSION  
AJ277206  
VERSION  
AJ277206.1 GI:7340730  
KEYWORDS  
s-adenosylmethionine synthetase.  
SOURCE  
Camellia sinensis  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; Ericales; Theaceae; Camellia.  
REFERENCE  
1  
Feng, Y.F. and Liang, Y.R.  
Cloning of s-adenosylmethionine synthetase gene in tea plant  
Unpublished  
2 (bases 1 to 1776)  
Feng, Y.F.  
Direct Submission  
Submitted (27-MAR-2000) Feng Y.F., Tea Department, Hua jia chi  
Campus, Zhe jiang University, 310029, CHINA  
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Location/Qualifiers  
1..1776  
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S"  
CDS  
ORIGIN

Query Match 57.3%; Score 850.4; DB 8; Length 1776;



Best Local Similarity 82.9%; Pred. No. 2.5e-212; Matches 982; Conservative 0; Mismatches 201; Indels 1; Gaps 1;			
Qy	80	GAGACATTCCTATTATTACCTCAGAGTCAGTGAACGAGGAGCACCCCTGACAAAGCTCTGCGAC	139
Db	116	GAGACTTTTCTATTTCACATCCGATCTGTGATGAGGGTCACCCAGACACAGCTCTGTGAT	175
Qy	140	CAAAATCCGATGCTGTCTCGACGCTTGCTTGAACAGGACCCAGACCAAGGTTGCC	199
Db	176	CAGATATCTGATGCAGTTCTCGATGCTGCTTGAAACAAGATCAAGACAGCAAGATTGCC	235
Qy	200	TGGAAACATGCAACCAAGACCAACTTGGTCATGGTCTTTCGGAGAGATCACCAAGGCCC	259
Db	236	TGTGAGACTTTGCACCAAGACTTAACATGGTCATGGTCTTCGGTGAATTCACAAACCAAGCC	295
Qy	260	AACGTTCCACTACGAGAAGATGTCGCTGACACCTGCAAGAACATCGGCTTCGTCTCAAAAC	319
Db	296	GCGGTAGACTATGAGAAGATTGTGCGTGAACATGCGCGACCAATGGATTGTGTTTCCGAT	355
Qy	320	GATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACAATTGAGCAGCAGAGCCCT	379
Db	356	GATGTTGGTCTTGATGCTGATAATTGCAAGTTCTAGTCAACATCGAGCAACAGAGCCCT	415
Qy	380	GATATTGCCACGGGTGTCAGGGCACTTACAAAAGACCCGAGGAAAATCGGTGCTGGGA	439
Db	416	GATATTGCCACGGGTGTCAGGGTCATCTCACTAAGCGCCCGAGGAGATTGGTGCCGGT	475
Qy	440	GACCAGGTCACATGTTTGGTATGCCCACGAGCAAAACCCAGAAATGTATGCCAATTCGAT	499
Db	476	GACCAGGTCACATGTTTGGTATGCCCACAGATGAACATTCCTCGAGCTGATGCCCTCAGC	535
Qy	500	CATGTTCTTGCAACTAAACTCGGTGCTGCTCACCGAGGTTGCCAAGAACGGAACCTGC	559
Db	536	CATGCTCTTGCAACCAACTTGGTGGCGGCTCACTGAAGTCGCAAGAAATGGAACCTTGC	595
Qy	560	CCATGGTTGAGGCTTGATGGGAAAACCCAAAGTGACTGTTGAGTATTTAACAATGACAAACGGT	619
Db	596	CCCTGGTTAAGACCTGATGGCAAAACCCAAAGTGACTGTTGAGTATTTAACAATGAGAAAGGT	655
Qy	620	GCCATGGTCCAGTTGCTGTGTCACATGTCGTTATCTCCACCACCAATGATGAGACGTG	679
Db	656	GCCACGGTTCCTATTTCGTGTGCAACACCCCTTCTCATCTCCACCCAAACAGATGAGACCGTG	715
Qy	680	ACCAACGACGAAATTTGACGTGACTCAAGGAGCATGTGATCAAGCCGGTGATCCCCGGAG	739
Db	716	ACAAATGATGAGATTGCTGTGATCTTTAAGAGCATGTCTCATCAAGCTGTTATCCCGAC	775
Qy	740	AAGTACCTTGATGAGAAGACATTTTCCAATTGAACCCCTCTGGCCGTTTGTCAATTGGA	799
Db	776	AAGTATCTGATGAGAAGACCATCTTCCACCTCAACCTTCTGGTCGCTTGTCTATTGGC	835
Qy	800	GGTCTTCAACGGTGATGCTGTCTCACCGCGCGAAGATCATCTCGATCTTACCGGAGGA	859
Db	836	GGACCTCATGGCGATGCTGGTCTACCTGGCGCGAAGATCATCATCGACATTTACGGTGGG	895
Qy	860	TGGGGTGCTCATGGTGGTGGTGTCTTCTCCGGGAAGGATCCCAACCAAGGTTGATAGAGT	919
Db	896	TGGGGTGCTCATGGTGGTGGTGTCTTCTCCGGAAGGACCCCAACCAAGGTTGATAGAGT	955
Qy	920	GGTGCTTTACATTTGAGACAGGCTGCTTAAGAGCAATTTGGCAAGTGAAGTCCAGCAAGG	979
Db	956	GGAGCATACATTTGTCAGCGAGGCTGCGAAGAGCATCGTGGCCAATGGCTTGGCGGAGG	1015
Qy	980	TGCATTTGCAAGTGTCTTATGCCATTTGGTGTGCCCAGCCCTTGTCTGTCTTTGTTGAC	1039
Db	1016	TGCATTTGTCAGGTTTCTTACGCCATTTGGTGTCTTCTGAGCCATTTGTCGGTTTTGCTGGAC	1075
Qy	1040	ACCTATGGCACCGGGAAGATTCATGATAAGGAGATTCTCAACATTTGTGAAGGAGAACTTT	1099
Db	1076	ACGTATGGGACTGGGAAGATTCGGGACAAAGAGATTCTCAAGATTGTGAAGAGAGCTTTT	1135
Qy	1100	GATTTACGGCCCGGTATGATCTCCATCAACCTTGGATCTCAAGAGGGGTGGGAATAACAGG	1159

Db	1136	GATTTTAGGCTGGCATGATGGCATCAACCTTGATCTGAGAGGGCGGCAACAGTAGG	1199
Qy	1160	TTCTTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCTGACTTTCATCGG-A	1218
Db	1196	TTCTTTGAAGACTGCTGCCTATGGACATTTTGGCAGGATGATCCTGACTTCACATGGAA	1255
Qy	1219	AGTGGTCAAGCCCTCAAGTGGGAGAGGCGCTTAAGGCCATTCTAT	1262
Db	1256	AGTGGTGAAGCCCTCAAGTGGGACAAACCTCAAGCTAATTCCT	1299
RESULT 13			
LOCUS	AP004964	7894 bp DNA linear	PLN 22-JUL-2003
DEFINITION	Lotus corniculatus var. japonicus genomic DNA, chromosome 1, clone:LjT20J05, TM0143a, complete sequence.		
ACCESSION	AP004964		
VERSION	AP004964.1	GI:21907982	
KEYWORDS	HTG.		
SOURCE	Lotus corniculatus var. japonicus (Lotus japonicus)		
ORGANISM	Lotus corniculatus var. japonicus		
REFERENCE	1		
AUTHORS	Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Sato,S. and Tabata,S.		
TITLE	Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb Regions of the Genome		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 7894)		
AUTHORS	Nakamura,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ytn@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)		
FEATURES	Location/Qualifiers		
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ORIGIN			
Query Match	57.2%	Score 849.8; DB 8; Length 7894;	
Best Local Similarity	81.6%;	Pred. No. 4.8e-212;	
Matches	996; Conservative	0; Mismatches 222; Indels 3; Gaps 1;	
Qy	33	CTCTGCTCTTCTTCTACCTTTTCAAGTTTAAAGTATTAAAGATGGCAGAGACATTCCTAT	92
Db	245	CTGACTCTTTCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT	304
Qy	93	TTACTCTCAGAGTCAGTGAACGAGGGACACCTCTGACAAGCTCTCGACCAAAATCTCCGATG	152
Db	305	TCACCTCTGAATCTGTAACAGGGGTCAACCTGACAAGCTGTGCGACCATCTCCGATG	364
Qy	153	CTGTCCTGACGCTTGCTTGAACAGGACCCAGACAGCAAGTTGGCTGCGAAACATGCA	212
Db	365	CGGTGCTCGATGCCTGTCTAGACAGGATCCTGACACAGGTTGGCTGTGAGACTTGCA	424
Qy	213	CCAAGACCAACTTGGTCATGCTCTTCGGAGAGATCACCACCAAGGCCAACGTTTGACTACG	272
Db	425	CCAGACTAACATGGTCATGGTCTTTTGGAGAGATCACACCAAGGCCAACGTTGACTATG	484
Qy	273	AGAGATCGTCGGTGACACCTGCGAGNAACATCGGCTTCGTCTCAACAGATGTGCGACTTG	332



485 AGAAGATCGTCCGTGACACGTCGCGTACATCGATTCGTTGATGATGGTCTCTTG 544  
333 ATCTGACAACTCAAGGCTCTTTGTAACATTGAGCAGACGACCTGATATTGCCCCAG 392  
545 ATGCTGACAAATGCAAGGCTCTGTTGACATTTGAGCAGACGACCTGATATTGCTCAG 604  
393 GTGTGACGCGCCACCTTACAAAGACCCGAGAAATCGGTGCTGGAGACCAAGGCTACA 452  
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513 CTAACCTCGGTGCTGCTCACCGAGGTTGCAAGAACGGAACCTGCCCATGTTGAGGC 572  
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1442 TCAAGTGGGAGAGCTCAAG 1462

RESULT 14  
CRSAMS2  
LOCUS  
DEFINITION  
ACCESSION

CRSAMS2 1381 bp mRNA linear PLN 12-FEB-1997  
C.roseus mRNA for S-adenosyl-L-methionine synthetase 2.  
271272

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

271272.1 GI:1655577  
methionine adenosyltransferase; S-adenosyl-L-methionine synthetase.  
Catharanthus roseus (Madagascar periwinkle)  
Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Gentianales; Apocynaceae; Rauvolfioideae;  
Vincaceae; Catharanthus.  
1 (bases 1 to 1381)  
Schroeder, G., Eichel, J., Breinig, S. and Schroeder, J.  
Three differentially expressed S-adenosylmethionine synthetases  
from Catharanthus roseus: molecular and functional characterization  
Plant Mol. Biol. 33 (2), 211-222 (1997)  
97188555  
9037140

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
TITLE

Direct Submission  
Submitted (18-APR-1996) Schroeder J., University of Freiburg,  
Institut fuer Biologie II, Schaenzlestr. 1, D-79104 Freiburg,  
GERMANY

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source

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pp<sub>i</sub> + Pi"

gene

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ORIGIN

Query Match 57.1%; Score 848.6; DB 8; Length 1381;  
Best Local Similarity 80.3%; Pred. No. 7.2e-212;  
Matches 995; Conservative 0; Mismatches 244; Indels 0; Gaps 0;  
QY 19 CACCACACACTCTCTCTGCTCTTCTTACCTTTCAAGTTTAAAAAGTATTAAAGTGC 78  
DB 6 CTCGATTTCTCTCGTTGCTCTGCCCTGCTCCATCTGTCTACCGCAAGTTTAGAAGGAT 65  
QY 79 AGAGACATTCCTATTATCTCAGATCAGTGAACGAGGACACCTCTGACAGCTCTGCGA 138  
DB 66 GGAGACCTTTTGTTCACATCTGAGTCGCGTGAATGAGGACACCTCTGATAGCTTTGTA 125  
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199 QY CTCGGAACATGACCAAGACCAACTTGTGTCATGTCTTCGAGAGATCACCAACAGGC 258  
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259 QY CAACGTTGACTACGAGACATCGTGTGACACCTGCGAGACATCGGCTTGTCTCAA 318  
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559 QY CCATGTTGAGCCCTGATGCGGAAACCCCAAGTACTGTTGATGATTTACAATGACACCG 618  
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619 QY TGCCATGTTTCCAGTTTCGTTGTCACACTGCTGCTTATCTCCACCCCAACATGATGACTGT 678  
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739 QY GAAGTACCTTGATGAGAACCATTTTCCACTGAAACCCCTCTGGCGTTTGTCTATTGG 798  
726 Db GAAGTACCTTTGATGAGAACCATATTTCCACTTGAATCTCTGACGCTTTGTTATTGG 785  
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906 Db TGGTGCTTATATTTGTAGCAAGCTGCAAGAGCATTTGTCAGTGTGCTTTGCGCCGAG 965  
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1146 Db GTTCTTTGAAGACTGCGCGCTTATGACATTTTCGCTAGAGAGGATCTGACTTCACTATGGA 1205  
1219 QY AGTGTTCAGGCCCTTCAAGTGGGAGAGGCCCTTAAGGCCA 1257  
1206 Db AGTGTTCAGGCCCTTCAAGTGGGAGAGGCCCTTGAAGCCTA 1244

RESULT 15  
MCU79767  
LOCUS  
DEFINITION  
Mesembryanthemum crystallinum methionine adenosyltransferase mRNA,  
complete cds.  
ACCESSION  
U79767  
VERSION  
U79767.1  
KEYWORDS  
GI:1724103  
ORGANISM  
Mesembryanthemum crystallinum (common iceplant)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Aizoaceae; Mesembryanthemum.  
1 (bases 1 to 1628)  
Direct Submission  
Submitted (26-NOV-1996) Biochemistry, University of Arizona, Bio  
Sciences West 513, Tucson, AZ 85721, USA  
Location/Qualifiers  
1. 1628  
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ORIGIN  
Query Match 57.1%; Score 847.6; DB 8; Length 1628;  
Best Local Similarity 83.2%; Pred. No. 1.4e-211;  
Matches 977; Conservative 0; Mismatches 194; Indels 3; Gaps 1;  
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Db 132 CAGATCTCTGATGAGTTCCTTGTATGCTTGCCTTGCCTGAGATGCTGAGCAAGGTTGCT 191  
QY 200 TCGCAAAACATGCACCAAGACCAACTTGTGTCATGCTTTCGAGAGATCACCAACAGGCC 259  
Db 192 TGTGAGACTTGTAACAGACCAACTTGTGTCATGCTTTCGCTGAGATCACCAACAGGCC 251  
QY 260 AACGTTGACTACGAGAAGATCGTGTGACACCTTGCAGGAAACATCGGCTTCTCTCAAC 319  
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492 CATGTCCTTCTGTACCAAGCTTCGGTGGCCGCTTGACCGAGGTCCGTAAGAAGACGGAACCTGC 551
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Search completed: August 31, 2005, 06:01:19  
Job time : 6551.49 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 18:40:09 ; Search time 816.183 Seconds  
(without alignments)  
10770.640 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1485	100.0	1485	2	AAX07184 Soybean S
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4	822.8	55.4	1190	8	ADA69525 Rice gene
5	819.8	55.2	1191	12	ADJ44928 Plant cDN
6	819.6	55.2	1582	2	AAX07183
7	813.4	54.8	1190	8	ADA70676 Rice gene
8	804.4	54.2	1521	3	AAC45478 Arabidops
9	802.8	54.1	1508	3	AAC33986 Arabidops
10	796.4	53.6	1182	8	ADA67853 Arabidops
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14	783.6	52.8	1395	3	AAC33674 Arabidops
15	778.6	52.4	1182	2	AAT99143
16	777.8	52.4	1380	2	AAX07185 Wheat S-a
17	777	52.3	1182	2	AAT99142
18	755.2	50.9	1674	3	AAC47744 Zea mays
19	745.2	50.2	1636	5	AAD02296 Nicotiana
20	729.2	49.1	1173	6	ABZ14640 Arabidops

21	729.2	49.1	1653	3	AAC45944 Arabidops
22	715.6	48.2	1654	3	AAC35348 Arabidops
23	468.4	31.5	725	9	ACL15153 DNA clone
24	458.8	30.9	622	13	ACN49337 Cotton pr
25	458.2	30.9	710	9	ACL15154 DNA clone
26	457.2	30.8	618	13	ACN50650 Cotton an
27	443.8	29.9	522	3	AAA51039 Partial s
28	427	28.8	1185	13	ADSL17323 Rat liver
29	422.8	28.5	676	9	ACL15152 DNA clone
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35	422.4	28.4	2828	13	ADQ91617 Human met
36	422.4	28.4	2828	13	ACN37730 Tumour-as
37	420.8	28.3	1283	5	AAC91225 Human met
38	420.8	28.3	1283	11	ADI32045 Human CDN
39	419.6	28.3	3495	12	ADL12741 Human ste
C 40	419.2	28.2	672	9	ACL15221 DNA clone
C 41	418.8	28.2	617	9	ACL15210 DNA clone
C 42	418.8	28.2	1840	10	ADB59179 Toxicity-
C 43	418.8	28.2	1840	10	ADB53879 Primary r
C 44	416.6	28.1	631	9	ACL15198 DNA clone
C 45	414.4	27.9	623	9	ACL15211 DNA clone

ALIGNMENTS

RESULT 1  
AAX07184  
ID AAX07184 standard; cDNA; 1485 BP.

AC AAX07184;

DT 21-MAY-1999 (first entry)

DE Soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.

KW S-adenosylmethionine synthetase; soybean; amino acid; lysine; threonine;  
methionine; cysteine; isoleucine; transgenic plant; crop improvement;  
KW food; feedstuff; ss.

OS Glycine max.

Key Location/Qualifiers  
CDS 74..1252  
FT /\*tag= a

PN WO9855601-A2.

PD 10-DEC-1998.

XX 05-JUN-1998; 98WO-US011692.

XX 06-JUN-1997; 97US-0048771P.

XX 12-JUN-1997; 97US-0049443P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Allen SM, Rafalski JA, Hitz WD, Kinney AJ, Abell LM;

XX Thorpe CJ;

XX WPI; 1999-070263/06.

XX P-PSDB; AAW97743.

XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -

XX PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine

XX PT synthase; threonine deaminase; S-adenosylmethionine synthetase.

XX Claim 44; Page 66-67; 98pp; English.





RESULT 3	PR	18-JUN-1999;	99US-0139459P.
AAC33535	PR	18-JUN-1999;	99US-0139460P.
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17-OCT-2000 (first entry)	PR	21-JUN-1999;	99US-0139817P.
XX	PR	22-JUN-1999;	99US-0139899P.
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KW Hybridisation assay; genetic mapping; gene expression control;	PR	24-JUN-1999;	99US-0140695P.
KW protein identification; signal transduction pathway; metabolic pathway;	PR	28-JUN-1999;	99US-0140823P.
KW promoter; termination sequence; ss.	PR	29-JUN-1999;	99US-0140991P.
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PN	PR	02-JUL-1999;	99US-0142055P.
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PD	PR	08-JUL-1999;	99US-0142803P.
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PF	PR	12-JUL-1999;	99US-0142977P.
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PR	01-SEP-1999;	99US-0151930P.	QY	440	GACCAAGGTCACATGTTGGCTATGCCACGACGAAACCCAGAAATTTGATGCAATTTGAGT	499
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PR	10-SEP-1999;	99US-0153070P.	QY	500	CATGTTCTTGCAACTAACTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	559
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PR	06-OCT-1999;	99US-0157865P.	Db	853	GGACCCCATGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	912
PR	07-OCT-1999;	99US-0158029P.	QY	860	TGGGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	919
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Best Local Similarity 76.7%; Pred. No. 5.5e-229;  
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Db 133 GAGACTTTTCTATTTACATCTGAGTCTGTAAAGAGGAGACCCACAGCTCTGTGAC 192  
QY 140 CAAATCTCGATGCTGCTGCTGAGCGCTTGGCTTGAACAGACCCAGAGAGAGGTTGCC 199  
Db 193 CAGATCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252  
QY 200 TCGGAAACATGACCAAGACCACTTGGTCAATGCTTCCGAGAGATCAACCAAGGCC 259  
Db 253 TGTGAGACATGACCAAGACCAACATGGTCAATGCTTGGTGGAGATCACTACCAAGGCT 312

Db 1392 TTTGTTTATGATCATTTGTTACTTGAGCTATTTTCAATTGGGTGTTTGTGTTTATGGCGAC 1451  
QY 1400 TTTTACATG 1408  
Db 1452 TTTTACACG 1460

RESULT 4  
ADA69525  
ID ADA69525 standard; DNA; 1190 BP.  
XX  
AC ADA69525;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 2848.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
XX WPI; 2003-175290/17.  
XX  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
XX Claim 6; SEQ ID NO 2848; 899pp; English.  
XX  
XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
XX Sequence 1190 BP; 269 A; 330 C; 328 G; 263 T; 0 U; 0 Other;  
SQ

Query Match 55.4%; Score 822.8; DB 8; Length 1190;  
Best Local Similarity 81.2%; Pred. No. 1.2e-228;  
Matches 956; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

QY 80 GAGACATTCCTATTACCTCAGATCAGTGAACGAGGACACCCCTGACAGCTCTGCGAC 139  
Db 13 GATACCTTCCTCTTTACCTCGAGTCTGTGAACGAGGACACCCCTGACAGCTCTGCGAC 72  
QY 140 CAAATCTCCGATGCTGCTCCTCGACGCTTGCCTTTGAACGAGACCCAGCAAGGTTGCC 199  
Db 73 CAACTCTCAGATGCTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132  
QY 200 TCGAAACATGCACCAAGACCAACTTTGGTTCATGGTCTTCGAGAGATCAACCAAGGCC 259  
Db 133 TGTGAGACCTGCACCAAGACCAACTTTGGTTCATGGTCTTCGAGATCAACCAAGGCT 192

QY 260 AACGTTGACTACGAGAGATCGTGGTGACACCTGCAGGAACATCGGCTTGGTCTCAAAC 319  
Db 193 AACGTTGACTATGAGAAGATTGTCAAGGAGACATCGCGTAACATCGGTTTGTGTGAGCT 252  
QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCTCTTTAAACATTTGACGACGAGCCCT 379  
Db 253 GATGTGGTCTCGATGCTGACCACTGCAAGGTGCTTTGNAACATCGAGCAGTCCCT 312  
QY 380 GATATTGCCAGGGTGTGCA CGGCCACCTTACCAAAAGACCCGAGGAATCGTGTCTGGA 439  
Db 313 GACATTGCACAGGGTGTGACGGGCACCTTACCAGCGCCCTGAGGAGATTGGTGTCTGGT 372  
QY 440 GACAGGGTCAATGTTTGGCTATGCCACGACGAAACCCAGAAATTCATGCAATGAGT 499  
Db 373 GACAGGGGACACATGTTTGGATATGCAACTGATGAGACCCCTGATGTCCTCCCTCAGC 432  
QY 500 CATGTTCTTGCAACTAAACTCGTGCTCGTCTCACCGAGGTTTCGCAAGAACCGACCTGC 559  
Db 433 CATGCTCTTGCTACCAAGCTTGGCGCTGCTTACGGAGGTTTCGCAAGATGGGACCTGC 492  
QY 560 CCATGGTTGAGGCTGATGGGAAAACCCAAAGTACTGTTGAGTATTACAATGACAAAGGT 619  
Db 493 GCATGGCTCAGGCTGACGCGGAAGACCCCAAGTACTGTTGAGTACCGCAATGAGAGCGT 552  
QY 620 GCCATGGTTCCAGTTCGTGTCACACTGCTTATCTCCACCCACATGATGAGACTGTG 679  
Db 553 GCCAGGGTCCCTGCTCGGTGTCACACCGCTCTCATCTTACCAGCATGATGAGACAGTC 612  
QY 680 ACCAACGACGAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739  
Db 613 ACCAACGATGAGATTGCTGCTGACCTGAAGGAGCATGTGATCAAGCCCTGTATCCCGAG 672  
QY 740 AAGTACCTTGATGAGAGACCAATTTTCCATTGAAACCCCTCTGGCGGTTTGTCTATTGGA 799  
Db 673 CAGTACCTTGATGAGAGACCAATTTTCCATTGAAACCCCTCTGGTGTGCTGCTGCTGCTGCT 732  
QY 800 GGTCTCTACGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859  
Db 733 GGACCTCATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792  
QY 860 TGGGGTGTCTATGGTGTGCTGCTTCTCCGGGAGGATCCCAAGGTTGATAGGAGT 919  
Db 793 TGGGGAGCTCACGGTGTGCTGCTTCTCTGCAAGGACCCCAAGGTTGACCGCAGT 852  
QY 920 GGTGCTTACATGTGAGACAGCTGCTTAAGACATTTGGCAAGTGGGACTAGCCAGAGG 979  
Db 853 GGAGCATACGTGCGCAAGGCAAGCTGCCAAGAGCATTTGTTGCTAGTGGGCTTGTCTGCGCGC 912  
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTGCTGCTGCCGAGCCCTTGTCTGTCTTTGTTGAC 1039  
Db 913 TGCAATTGTCCAAGTATCATAGCCATCGGTGTCCAGAGCCACTGTCTGATTTCTGTCAC 972  
QY 1040 ACCTATGTCACCGGAGAGATCCATGATGAAGAGATTCTCAACATTTGTAAGAGAGAACTTT 1099  
Db 973 ACATACGGCACTGCGCAGGATCCCTGACAAAGGAGATCCTCAAGATTGTGAAGGAGAACTTC 1032  
QY 1100 GATTTACGGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGATTAACAGG 1159  
Db 1033 GACTTCAGGCTCGGCATGATCATCATCAACCTTGTACCTCAAGAAAGGCGGCAACGGACGC 1092  
QY 1160 TTCTTGAAGACTGTCTGATATGGACATTTCCGACAGAGAGGCCCTTGACTTTCACATGGGAA 1219  
Db 1093 TACCTCAAGACGGCGCTTACGGTCACTTCGGAAGGAGACCCACAGACTTTCACCTGGGAG 1152  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGCCCTTAAGGCCA 1257  
Db 1153 GTGGTGAAGCCCTCAAGTGGGAGAGCCCTTCTGCTA 1190

RESULT 5  
ADJ44928  
ID ADJ44928 standard; cDNA; 1191 BP.



QY 1160 TTCTTGAAGACTGCTGCATATGACACACTTGGGAGAGAGACCCTGACTTACATGGGAA 1219  
Db 1093 TACCTCAAGACGCGGCTTTACGGTCACTTCGGAAGGAGACGCCAGACTTCACTGGGAG 1152  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCA 1257  
Db 1153 GTGGTGAAGCCCTCAAGTGGGAGAGAGCCCTTCTGCCTA 1190

RESULT 6

AAX07183

ID AAX07183 standard; cDNA; 1582 BP.

XX

AC AAX07183;

XX 21-MAY-1999 (first entry)

XX

DE Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.

XX S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;

KW threonine; methionine; cysteine; isoleucine; transgenic plant;

KW crop improvement; food; feedstuff; ss.

XX

OS Zea mays.

XX

FH Key Location/Qualifiers

FT CDS 140..1330

FT /\*tag= a

FT

XX

PN W09855601-A2.

XX

PD 10-DEC-1998.

XX

PF 05-JUN-1998; 98WO-US011692.

XX

PR 06-JUN-1997; 97US-0048771P.

PR 12-JUN-1997; 97US-0049443P.

XX

PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX

PI Falco SC, Allen SM, Rafalski JA, Hitz WD, Kinney AJ, Abeil LM;

PI Thorpe CJ;

XX

XX WPI; 1999-070263/06.

DR P-PSDB; AAW97742.

XX

PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -  
PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine  
PT synthase; threonine deaminase; S-adenosylmethionine synthetase.

XX

PS Claim 41; Page 62-63; 98pp; English.

XX

XX This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which codes  
CC for a full-length corn S-adenosylmethionine synthetase (see AAW97742).

CC The clone was isolated from a corn callus cDNA library and identified by  
CC comparison to public sequence databases using BLAST algorithms. It shows  
CC sequence similarity to the Oryza sativa enzyme. The invention relates to  
CC new isolated nucleic acid fragments (see AAX07168-85) encoding plant  
CC enzymes (see AAW9772-44) that catalyse steps in the biosynthesis of  
CC lysine, threonine, methionine, cysteine and isoleucine from aspartate,  
CC the enzyme being selected from dihydropicolinate reductase,  
CC diaminopimelate epimerase, threonine synthase, threonine deaminase or S-  
CC adenosylmethionine synthetase. The invention also relates to the  
CC construction of a chimeric gene encoding all or a portion of the  
CC biosynthetic pathway enzyme, in sense or antisense orientation, where  
CC expression of the chimeric gene results in production of altered levels  
CC of the enzyme in a transformed host cell. Overexpression or reduction of  
CC expression of genes encoding the amino acid biosynthetic pathway enzymes  
CC in crop plants such as corn, soybean and wheat can be used to alter  
CC levels of the amino acids in human food and animal feed. Transformed host  
CC cells can also be used to identify compounds that inhibit one of the  
CC enzymes

XX Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 U; 0 Other;  
SQ  
Query Match 55.2%; Score 819.6; DB 2; Length 1582;  
Best Local Similarity 81.0%; Pred. No. 1.2e-227;  
Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACCCCTGACAAGCTCTGCCAC 139  
Db 152 GACACCTTCTCTTCACTCGGAGTCTGTGAACGAGGAGACCCCTGACAAGCTCTGCCAC 211  
QY 140 CAAATCTCCGATGTCTCTCGAGCTTGTCTTGAACAGGACCCGAGAGCAAGGTTGCC 199  
Db 212 CAGGTCTCAGATGCGCTTCTTGAAGCTTGTCTGAGGACCCCTGAGCAAGGTTGCT 271  
QY 200 TCGAACAATGACCAAGACCAACTTGTCTATGTCTTTCGGAGAGATCACCAACGAGCC 259  
Db 272 TGTGAGACCTGCACCAAGACCAACTGTGTCTATGTCTTGTGTGAGATCACCAACGAGCC 331  
QY 260 AACGTTGACTAGGAGAGATCGTGGTGACACCTGCAGGACACATCGGCTTCTCTCAAC 319  
Db 332 AATGTCGACTACGAGAAGATTGTGAGGAGACCTGCCGCAACATTTGGTTTGTGTCAAC 391  
QY 320 GATGTGGACTTGTATGCTGACAACTGCAAGGTCTTGTAAACATTTGACGACGAGCCCT 379  
Db 392 GATGTGGGCTTGACGCTGACCACTGCAAGGTCTGCTGAACATTTGACGACGAGTCCCT 451  
QY 380 GATATTGCCAGGCTGTCACGCGCACTTACCAAGACCCGAGAGAAATCGGTCTGGA 439  
Db 452 GATATTGCTCAGGGTGTGATGGCCACTTCAACGAGCCCGAGGAGATTGGAGCTGT 511  
QY 440 GACGAGGTACATGTTTGGCTATGCCAGCGAGAAACCCAGATTTCATGCAATTGAT 499  
Db 512 GACCAGGAGACATGTTTCGGGTATGCGACCCATGAGACCCCTGAGTTGATGCCCTCAGC 571  
QY 500 CATGTTCTTGCAACTTAACTCGGTCTGCTCTCACCGAGGTTGCGAAGAACGGAACCTGC 559  
Db 572 CATGTTCTTGCCACCAAGCTAGGTGCTCTCTCACCGAGGTCCGCAAGAACGGAACCTGC 631  
QY 560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGAGTATTCAATGACAAACGGT 619  
Db 632 CCCTGGCTCAGGCTGATGGGAAAGCCCAAGGTGACAGTCTGAGTACCGCAATGAGGCTGT 691  
QY 620 GCCATGGTTCCAGTTTCAGTCCACACTGCTTATCTCCACCACATGATGAGACTGTG 679  
Db 692 GCCATGGTCCCATCCGTTCCACACCTCTCATCTCCACCACGACGACGAGACAGTGT 751  
QY 680 ACCAACGACGAAATTCGACGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739  
Db 752 ACCAATGATGATGCTGCTGACCTGAAGGAGCATGTCTCAAGCCCTATCATCCCTGAG 811  
QY 740 AAGTACCTTGATGAGAAGACCATTTTCCATTGAACCCCTCTGGCCGCTTTGTCTATTGGA 799  
Db 812 CAGTACCTTGACGAGAAGACCATTTTCCACCTTTAACCCATCCGCGCGCTTTGTCTATTGT 871  
QY 800 GGTCTCAGGCTGATGCTGGTCTCACCGCCGCGAGATCATCATCATGATTTTACCGAGGA 859  
Db 872 GGACCTCAGCGGATGCTGGCTCTACTGCGCGCAAGATCATCATTTGACACCTTACCGTGGC 931  
QY 860 TGGGCTGCTCATGTGTGTGTGCTTTCTCCGGGAGAGATCCCAACGAGTTGATAGGAGT 919  
Db 932 TGGGAGGCCATGGCGGTGGCGCTTTCTCCGGCAAGGACCCCAACCAAGGTTGACCCGAGC 991  
QY 920 GGTGTTTACATTTGAGACAGCTGCTTAAGAGCATTTGGCAAGTGGAGTAGCCAGAGAG 979  
Db 992 GGAGCCTATGTCGGAGGAGGCTGCCAAGAGCATCTGTCGCGAGCGGCTTGTCTCGCGCG 1051  
QY 980 TGCATTGTGCAAGTCTCTTATGSCCATTTGTGCGCCGAGCCCTTCTCTGTCTTTCTGTGAC 1039  
Db 1052 GCCATGCTCCAGGTGCTCTAGCCATCGCGGTGCCGAGCCCTCTCTCGTGTCTTGTGAC 1111  
QY 1040 ACCTATGACCCGGGAGAGATTCATGATGAGGAGATTCTCAACATTTGTGAAGGAGAACTTT 1099



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Db      1149 GGAGGTGGTGAACCCCTCAAGTGGAGGACCTT 1183
RESULT 8
AAC45478
ID AAC45478 standard; DNA; 1521 BP.
XX
AC AAC45478;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46638.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
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PR 04-MAY-1999; 99US-0132484P.
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PR 14-MAY-1999; 99US-0134221P.
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PR 20-MAY-1999; 99US-0135124P.
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PR	04-OCT-1999;	99US-0157117P.	
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PR	14-OCT-1999;	99US-0159638P.	
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PR	21-OCT-1999;	99US-0160741P.	
PR	21-OCT-1999;	99US-0160767P.	
PR	21-OCT-1999;	99US-0160768P.	
PR	21-OCT-1999;	99US-0160770P.	
PR	21-OCT-1999;	99US-0160814P.	
PR	21-OCT-1999;	99US-0160815P.	
PR	22-OCT-1999;	99US-0160980P.	
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PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161406P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161922P.	
PR	28-OCT-1999;	99US-0161933P.	
PR	29-OCT-1999;	99US-0162142P.	
Query Match			54.2%; Score 804.4; DB 3; Length 1521;
Best Local Similarity			80.3%; Pred. No. 3.3e-223;
Matches 943; Conservative			0; Mismatches 231; Indels 0; Gaps 0;
QY	80	GAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGACACCCCTGACAAAGCTCTGCGAC	139
Db	91	GAATCTTTTGTTCATCATCTGAATCCGTCAACGAGGACATCCCGACAAAGCTTTGTGAT	150
QY	140	CAATCTCCGATGCTGCTCCGACGCTTCGACGAGCCGACAGAGCCGACAGCAAGGTTGCC	199
Db	151	CAGATCTCCGACGCTATCTCGATGCTTGCTTGAACAGAGCCCTGAGAGCAAGTTGCT	210





PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 54.1%; Score 802.8; DB 3; Length 1508;		
Best Local Similarity 80.2%; Pred. No. 9.5e-223;		
Matches 942; Conservative 0; Mismatches 232; Indels 0; Gaps 0;		
QY	80	GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 139
DB	93	GAATCTTTTGTTCACATCTGAATCCGTCAACGAGGGACATCCGACAAAGCTTTGTGAT 152
QY	140	CAAAATCCGATGCTGCTCCTGACGCTTCCTTGAACAGGACCCAGACAGCAAGGTGCGC 199
DB	153	CAGATCCGAGCGTATCCTCGATGCTTGCCTTTGAACAGACCCCTGAGAGCAAGTTGCT 212
QY	200	TCGAAACATGACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAACCAAGGCC 259
DB	213	TGTGAGACTTGTACCAAGACTAACATGGTTCATGGTTTGTGGAGAAATCACCAACCAAGGCT 272

RESULT 10  
ADA67853  
ID ADA67853 standard; DNA; 1182 BP.  
XX

QY	260	AACGTTGACTACGAGAAGATCGTGGTGACACCTCGAGGAAACATCGGCTTCGTCTCAAC 319
DB	273	AACGTTGATTACGAGCAGATTTGTTGTAATAACATGCGTGAGATTGGATTCTGTTCTGCT 332
QY	320	GATGTGGGACTTGTATGCTGACAACTGCAAGGTCCTTGTAAACATTTGACGAGAGCCCT 379
DB	333	GACGTTGGTCTAGATGCTGACAAATTGCAAGGTTCTGGTTAAACATTTGACGAGAGTCC 392
QY	380	GATATTGCCCCAGGCTGTGACGCGCCACCTTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
DB	393	GACATTGCAACAAGTGTTCATGGTCATCTCACCAAGAGCCAGAGAGGTTGGAGTGGT 452
QY	440	GACCAAGGTCACATGTTTGGCTATGCCACGAGCGAAACCCAGAAATTTGATGCAATTTGAGT 499
DB	453	GACCAAGGTCACATGTTTGGGTATGCTACTGATGAGACTCTCTGAGCTCATGCTCTTACT 512
QY	500	CATGTTCTTGCAACTAACTCGTCTGCTCACCGAGGTTCCGCAAGAACCGNAACCTGC 559
DB	513	CACGTTCTCGCTACTAAGCTTGGAGCTAACTCACTGAAGTTGCAAGAAATGGAACCTGC 572
QY	560	CCATGGTTGAGGCTCATGGGAAACCCCAAGTGACTGTTGAGTATTACAAATGACAAAGCT 619
DB	573	CCTTGGTTGAGGCGAGATGGTAAGACTCAAGTCACTATTGAGTACATCAACGNAAGCGA 632
QY	620	GCCATGGTTCCAGTTGCTGTCACACTGTGCTTATCTCCACCCAAACATGATGAGACTGTG 679
DB	633	GCCATGGTTCTGTACTGTCACACTGTTCTCATCTCAACACAGCATGACGAGACTGTG 692
QY	680	ACCAACGACGAAATTTGCAGCTGACCTCAAGGAGCATGTGNTCAAGCCGCTGATCCCGGAG 739
DB	693	ACTAAGCATGAGATCGCAGCTGATCTTAAGGAGCATGTGATCAAGCAGTGTATCCAGAG 752
QY	740	AAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGGCCGTTTGTTCATTGGA 799
DB	753	AAATACCTTGATGAGAAGAACCAATCTTCCATCTCAACCCATCTGTTGCTTTGTTATCGGA 812
QY	800	GGTCTCTCAGGTGATGCTGGTCTCACCGGCCAAGATCATCATCGATATTTACGAGAGA 859
DB	813	GGTCTCTCAGGATGTCAGGGCTTACCGGCCGTAAGATCATCATCGATATTTATGTTGCT 872
QY	860	TGGGCTGCTCATGGTGGTGGTCTTTCTCCGGGAAGGATCCCAACCAAGGTTGATAGGAGT 919
DB	873	TGGGCTGCACACGGAGGTGGTCTTTCTCTGGAAGGACCCCAACCAAGGTTGACAGGAGT 932
QY	920	GGTCTTACATTGTGAGACAGCTCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAGG 979
DB	933	GGGCTTACATCGTTAGGCAAGCAGCTAAGAGCATTTAGCAGTGGGCTAGCAGGCGG 992
QY	980	TGCATTGTGCAAGTGTCTTATGCCATTTGGTGTGCCGAGCCCTTCTCTGTTTGTGAC 1039
DB	993	GTCATTGTGCAAGTCTCGTATGCCATTGGTGTCCCTGAGCCATTCTCTGTGTTCTGTTGAC 1052
QY	1040	ACCTATGCAACGGGAAGATCCATGATTAAGAGATTCTCAACATTTGTGAGAGAGAACTTT 1099
DB	1053	AGTTATGGAACAGGAAGATACCAGAACGAGGATTTCTTGAGATTGTGAAGGAGAGTTT 1112
QY	1100	GATTTACGCGCGGTATCATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATAACAGG 1159
DB	1113	GATTTACGCGCAGGATGATCTCCATTAACCTTGGATCTGAAGAGAGGAGGTTATGGTAGG 1172
QY	1160	TTCTTGAAGACTGTGCTATATGGACATTTCCGACAGAGAGGCCCTGACTTCAATGGGAA 1219
DB	1173	TTCTTGAAGACTGTGCTATGTTGCTTACATTTGGAAGGAGCATGCTGATTTTCACTCTGGAG 1232
QY	1220	GTGTCAGGCCCTCAAGTGGGAGAGGCCCTAAG 1253
DB	1233	GTAGTCAAGCCACTCAAGTCTTAACAAAGGTCCAAG 1266

AC ADA67853;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Arabidopsis thaliana gene, SEQ ID 92.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
XX 22-JUN-2001; 2001WO-IB001105.  
PF  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
XX WPI; 2003-175290/17.  
DR  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 6; SEQ ID NO 92; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 1182 BP; 330 A; 283 C; 299 G; 270 T; 0 U; 0 Other;

Query Match 53.6%; Score 796.4; DB 8; Length 1182;  
Best Local Similarity 79.9%; Pred. No. 6.1e-221;  
Matches 938; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACACAGCTCTCGGAC 139  
DB 4 GAGACTTTCCTATTCATCTGAGTCTGTGAACGAGGACACCCCTGACAAAGCTTTTCGGAC 63  
QY 140 CAAATCTCCGATGCTGCTCCTCGACGCTTCGCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
DB 64 CAGATCTCTGATGCACTCTCTGATGCTGCTTGAACAGACCCCTGATAGCAAGTTGCT 123  
QY 200 TCGAAACATGACACCAAGACCAACCTTGGTTCATGCTTTCGAGAGATCAACCAAGGCC 259  
DB 124 TGTGAGACATGACCAAGACCAACATGGTTCATGGTTCGAGATCAACCAAGGCT 183  
QY 260 AACGTTGATACGAGAGATCGTGGTGACATCGTGCAGGAACATCGGCTTCCTCAAC 319  
DB 184 AGAATGATACGAGAGATGTCGCTGACATTCGCTGATTCATCTCTGAC 243  
QY 320 GATGTGGGACTTGATGCTGACAACTCAAGGCTTGTAAACATTCAGCAGCAGAGCCCT 379  
DB 244 GATGTTGGTCTTGATGCTGACAAATGCAAGTCTTGTAAATGAAACACAGAGCCCA 303  
QY 380 GATATTTGCCAGGTTGTGACGGCCACCTTACAAAGACCCGAGGAAATCGGTGCTGA 439  
DB 304 GACATTTGCTCAAGGTTGCTTCGCTGATCTTCAACCAACGTCAGAGACATTCGAGCTG 363

QY 440 GACCAGGCTCACATGTTTGGCTATGCCACGACGAAACCCAGAAATTCATGCTATTGAGT 499  
DB 364 GACCAGGACACATGTTTGGTTATGCCACTGATGAACCCCTGAGCTCATGGCTTTGAGT 423  
QY 500 CATGTTCTTGCAACTAACTCGGTCTCTCAACGAGGTTTCGCAAGAACGAACTGTC 559  
DB 424 CATGCTCTTGCAACCAAGATTTGGTCTCTCACTGAAGTCAGGAAGATGGAACCTTGC 483  
QY 560 CCATGGTTGAGGCTGATGGGAAACCAACCAAGTACTGTTGAGTATTACAATGACACCGT 619  
DB 484 CGTTGGTTAAGACCAAGATGGCAAGACCCCAAGTCACTGTTGAGTACTACAATGACAATGGC 543  
QY 620 GCCATGGTTCCAGTTCGTTCCACACTGCTTATCTCCACCCCAACATGATGAGACTGTG 679  
DB 544 GCTATGGTTCCAGTTCGTTCCACCGTCTGATCTCAACCCAGCAGATGAACCGTT 603  
QY 680 ACCAACGACGAAATTCGACGCTGACCTCAAGGAGCATGTGATCAAGCCCGTGTATCCCGGAG 739  
DB 604 ACCAATGACGAGATTTGCGCGTGACCTCAAGGAGCATGTGATCAAAACCAATCATCCAGAG 663  
QY 740 AAGTACCTTGATGAGAGAACCATTTTCACCTTGACCCCTCTGGCCGTTTGTCTATTGGA 799  
DB 664 AAATACCTTGACGACAAACCATCTTCACCTCAACCCATCAGGCCGCTTTGTGATCGGG 723  
QY 800 GGTCTCTACGCTGATGCTGGTCTCACCGGCGCAAGATCATCATCTTACCGAGGA 859  
DB 724 GGACACACGCTGATGCTGGTTAACTGGAGTGAAGATCATCATTCACATACGAGGA 783  
QY 860 TGGGCTGCTCATGTTGGTGGTCTTTTCCCGGAGGATCCCAACCAAGTTGATAGGAGT 919  
DB 784 TGGGAGCTCATGGAGTGGTGGTCTTCTCAGGCAAGACCCCAACCAAGTCCACAGAAGT 843  
QY 920 GGTGCTTACATGTCGACAGCGCTGCTAAGAGCATTTGTCAGAGGGTGGGAATTAACAGG 979  
DB 844 GGAGCTTACATCGTGAGGCAAGCAAGAGTGTGGTGGTAAATGGCATGGCTCGCAGG 903  
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTTGGTGTGCCGAGCCCTTGTCTGTCTTTGTTGAC 1039  
DB 904 GCTCTTGTGAGTCTCATAGCCATTTGGAGTACCCGAGCCATTTGTCTTCTGTTGAC 963  
QY 1040 ACCTATGTCACCGGAGAGATCCATGATGAAGAGATTTCTCAACATTTGTAAGAGAACCTTT 1099  
DB 964 ACTTACGGAACAGGGTTGATTCAGACAAAGAGATCCTGGAAGATCGTGAAGAGACATTC 1023  
QY 1100 GATTTACGCGCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATTAACAGG 1159  
DB 1024 GATTTACAGCCAGGAAATGATGACAACTTGGACTTTGAAGAGAGAGGAAATGGAAGG 1083  
QY 1160 TTCTTGAAGACTGCTGATATGACACTTTCGCGAGAGAGGACCCCTGACTTCACATGGGAA 1219  
DB 1084 TTTCAAGAAACGCGAGCGTATGGACATTTCCGAGAGAGACGACCCCTGACTTCACTCTGGAG 1143  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCCCTTAAG 1253  
DB 1144 GTGCTGAAGCCACTCAAGTGGGACAAACCTCAAG 1177

RESULT 11  
AAC46421  
ID AAC46421 standard; DNA; 1393 BP.  
XX  
AC AAC46421;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
XX promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
XX

PN	EP1033405-A2.	PR	01-JUL-1999;	99US-0142154P.
XX	PD	PR	02-JUL-1999;	99US-0142055P.
XX	06-SEP-2000.	PR	06-JUL-1999;	99US-0142390P.
XX		PR	08-JUL-1999;	99US-0142803P.
XX	25-FEB-2000; 2000EP-00301439.	PR	09-JUL-1999;	99US-0142920P.
PR	25-FEB-1999;	PR	12-JUL-1999;	99US-0143977P.
PR	05-MAR-1999;	PR	13-JUL-1999;	99US-0143542P.
PR	09-MAR-1999;	PR	14-JUL-1999;	99US-0143624P.
PR	23-MAR-1999;	PR	15-JUL-1999;	99US-0144005P.
PR	25-MAR-1999;	PR	16-JUL-1999;	99US-0144085P.
PR	29-MAR-1999;	PR	16-JUL-1999;	99US-0144086P.
PR	01-APR-1999;	PR	19-JUL-1999;	99US-0144325P.
PR	06-APR-1999;	PR	19-JUL-1999;	99US-0144331P.
PR	08-APR-1999;	PR	19-JUL-1999;	99US-0144332P.
PR	16-APR-1999;	PR	19-JUL-1999;	99US-0144333P.
PR	19-APR-1999;	PR	19-JUL-1999;	99US-0144334P.
PR	21-APR-1999;	PR	19-JUL-1999;	99US-0144335P.
PR	23-APR-1999;	PR	20-JUL-1999;	99US-0144352P.
PR	28-APR-1999;	PR	20-JUL-1999;	99US-0144632P.
PR	30-APR-1999;	PR	20-JUL-1999;	99US-0144884P.
PR	30-APR-1999;	PR	21-JUL-1999;	99US-0144814P.
PR	04-MAY-1999;	PR	21-JUL-1999;	99US-0145086P.
PR	05-MAY-1999;	PR	21-JUL-1999;	99US-0145088P.
PR	06-MAY-1999;	PR	22-JUL-1999;	99US-0145085P.
PR	06-MAY-1999;	PR	22-JUL-1999;	99US-0145087P.
PR	07-MAY-1999;	PR	22-JUL-1999;	99US-0145089P.
PR	11-MAY-1999;	PR	23-JUL-1999;	99US-0145192P.
PR	14-MAY-1999;	PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	PR	26-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	PR	27-JUL-1999;	99US-0145913P.
PR	18-MAY-1999;	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	PR	27-JUL-1999;	99US-0145919P.
PR	19-MAY-1999;	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	PR	04-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149929P.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	PR	27-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	PR	31-AUG-1999;	99US-0151308P.
PR	23-JUN-1999;	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	PR	07-SEP-1999;	99US-0152363P.
PR	24-JUN-1999;	PR	10-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	PR	16-SEP-1999;	99US-0154039P.

PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match 53.6%; Score 796.4; DB 3; Length 1393;

Best Local Similarity 79.9%; Pred. No. 6.7e-221;

Matches 938; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY	80	GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGAC	139
DB	98	GAGACTTTCCTATTACATCTGAGTCTGTGAACGAAGGACACCCCTGACAAAGCTTTGCGAC	157
QY	140	CAAACTCCGATGCTGTCTCGACGCTTGCCTTGAACGAGCCGACAGCAAGGTTGCC	199
DB	158	CAGATCTCTGATGCACTCTTATGCTGCTTGAACGAAGCCCTGATAGCAAGTTGCT	217
QY	200	TGGAAACATGACCAAGACCAACTTGGTCTTCGGAGAGATCACCAAGGACC	259
DB	218	TGTGACATGACCAAGACCAACATGGTCTATGGTTTCGGTGAGATCACCAAGGCT	277
QY	260	AACGTTGACTACGAGAAGATCGTGTGACACCTGCAGGAAACATCGGCTTCGTTCAAC	319
DB	278	ACGATTGACTACGAGAAGATTTGCCGTGACACTTGGCGTTCCATTGGATTCTCTGAC	337
QY	320	GATGTGGGACTTGACTGCACTGCAAGTCTTGTAAACATTTGAGCAGCAGGACCT	379
DB	338	GATGTGGTCTTGATGCTGACAAATGCAAAAGTCTTGTAAACATTTGAGCAGCAGC	397
QY	380	GATATTGCCAGGCTGTGACGCGCCACCTTACCAAAAGACCCGAGGAAATCGGTGTGGA	439
DB	398	GACATTGCTCAAGGTGTTTACCGGTCACTTACCAAAAGCTTCCAGAGACATTTGAGTGT	457
QY	440	GACCAAGGTCATGATTTTGGCTATGCGACGAGGAAACCCCAAGATTTGATGCAATGAGT	499
DB	458	GACCAAGGACACATGTTTGGTTATGCACTGATGAAACCCCTGAGCTCATGCTCTTGTAGT	517

QY	500	CATGTTCTTGCAACTAAACTCGTGCTCGTCTCACCGAGGTTGCAAGAACGAAACCTGC	559
DB	518	CATGCTCTTGCAACCAAGATTGGTGCTCGTCTCACTGAAGTCAGGAAGATGGAATCTGC	577
QY	560	CCATGGTTGAGCCCTGATGGGAAAAACCAAGTACTGTTGAGTATTACAATGACAAAGGT	619
DB	578	CGTTGGTTAAGACCAAGATGGCAAGACCAAGTCACTGTTGAGTACTACAATGACAAATGC	637
QY	620	GCCATGGTTCCAGTTCGTTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG	679
DB	638	GCTATGGTTCCAGTCCGTTGTCACACCGCTCTGATCTCAACCCAGCAGATGAAAACGTT	697
QY	680	ACCAACGACGAAATGACAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGAG	739
DB	698	ACCAATGACGAGATTGCGCGTGACCTCAAGGAGCATGTGATCAACCAATCATCCAGAG	757
QY	740	AAGTACCTTGATGAGAAGACCATTTTCCATTGAAACCCCTCTGGCCGTTTTGTTCATGGA	799
DB	758	AAATACCTTGACGACAAAACCATCTTCCACCTCAACCCATCAGGCCGTTTGTGATCGGG	817
QY	800	GCTCCTCAGGTCATGCTGGTCTCACCGCCGCAAGATCATCATCTGATCTTACCGAGA	859
DB	818	GGACCAACGCGTGTGCTGGTTAACTGCGACGTAAAGATCATCATTTGACACATACCGAGA	877
QY	860	TGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGT	919
DB	878	TGGGAGCTCATGGAGTGGTGGTCTTCTCAGGCAAGAGCCCAACCAAGTCGACAGAAGT	937
QY	920	GGTCTTACATTTGTGAGACAGGCTGTAAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAG	979
DB	938	GGAGCTTACATCGTGAAGCAAGAGAGAGTGTGGTGGCTTAATGGCATGGCTCGCAGG	997
QY	980	TGCATTGTCAAGTGTCTTATGCCATTGGTGTCCCGAGCCCTTTGTCTCTTGTTCAC	1039
DB	998	GCTCTGTCCAGGTCCTATACGCCATTTGGAGTACCCGAGCCATTGTCTCTTGTTCAC	1057
QY	1040	ACCTATGCGACCGGGAAGATCCATGATAAGAGAGATTCTCAACATTTGTAAGAGAGACTTT	1099
DB	1058	ACTTACGGAACAGGTTGATTTCCAGACAAAGAGATCCTGAGATCTGTGAAAGACATTC	1117
QY	1100	GATTTACGCCCCGCTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATACAGG	1159
DB	1118	GATTTACAGACAGGAAATGATGACAAATCACTTGGACTTGAAGAGAGGAGGAAATGGAAG	1177
QY	1160	TCTTGAAGACTGTGCATATGACACTTCCGACAGAGAGGACCTTGACTTCAATGCGGA	1219
DB	1178	TTTCAGAAAACGGCAGCGTATGACATTTCCGAAAGAGACGACCCCTGACTTCACTCGGAG	1237
QY	1220	GTGGTCAAGCCCTCAAGTGGGAGAAAGCCCTAAG	1253
DB	1238	GTCGTGAAGCCACTCAAGTGGGACAAACCTCAAG	1271

RESULT 12

AAT99141

ID AAT99141 standard; cDNA to mRNA; 1182 BP.

XX AAT99141;

AC AAT99141;

DT 26-MAR-1998 (first entry)

DE S-adenosylmethionine synthase 1 gene.

KW S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;  
sam1; ss.

OS Hordeum vulgare.

PN JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-00133406.



CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.

XX  
SQ Sequence 1185 BP; 235 A; 440 C; 346 G; 164 T; 0 U; 0 Other;

Query Match 53.0%; Score 786.4; DB 8; Length 1185;

Best Local Similarity 79.7%; Pred. No. 5e-218;

Matches 941; Conservative 0; Mismatches 236; Indels 3; Gaps 1;

QY	71	RAGATGGCAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTCGACAAG	130
Db	1	ATGGCGGGGAGACGTTCTCTTCACCTCCGAGTCGTTGAACGAGGTCACCCGGACAAAG	60
QY	131	CTCTGCGACCAATCTCCGATGCTGTCTCGACGCTTTCCTTGAACGAGACCCAGACAGC	190
Db	61	CTGTGGACACAGTGTGCGACGGGTCTCGACGGTCTCGCCAGGACCCCGACAGC	120
QY	191	AGGTTGCTCGGAACATGACCAAGACCACTTGTGTCATGGTCTTCGGAGAGATCAC	250
Db	121	AAAGTGGCTGGGAGACGTGTCACCAAGACCAACATGGTGTGTTCCGCGAGATCAC	180
QY	251	ACCAAGGCCAACGTTGACTACGAGAGATCGTGGTGACACCTGCGAGAACATCGGCTTC	310
Db	181	ACCAAGGCCAACGTCGACTACGAGAGATCGTGGTGACACCTGCGGCGATCGGCTTC	240
QY	311	GTCTCAAAACGATGCGGACTTGTATGCTGACAACTGCAAGTCTCTTGTAAACATTTAGCAG	370
Db	241	GTGTCCGACGCTCGGCTCGACCGGACCGCTGCAAGTCTCTGTCACATTCGAGCAG	300
QY	371	CAGAGCCCTGATTTGCCCAGGGTGTGACGGCCACTTACCAAGACCCGAGGAATC	430
Db	301	CAGTCCGCCGACATCGCGAGGGGTGACGGCCACTTCCAAAGCGCCCGAGGAGATC	360
QY	431	GGTGTGGAGACAGGGTCACATGTTTGGCTATGCGACGAGCAACCCAGAAATTTATG	490
Db	361	GGCGCGGGCGACAGGGCCACATGTTGGCTAGCCACCGACGAGNACCCCGAGCTGATG	420
QY	491	CCATTGAGTCATGTTCTTGCACAACTAACTCGGTGCTGCTTCAACGAGTTCGCAAGAAC	550
Db	421	CCCTCAGCAGCTCTCGCCACCAAGCTCGGCGCGCGCTCACCGAGTTCGCGAAGAAC	480
QY	551	GGAACTGCCATGTTGAGGCTGTATGGGAAACCCCAAGTGAATGTTGAGTATTACAT	610
Db	481	GGCACTGCGCTGCTGAGGCGCGACGCAAGCCAGCTCACCGTTCAGTACCTCAAC	540
QY	611	GACACGGTGCCATGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCCCAACATGAT	670
Db	541	GACCGCGGCGCATGTTCCCGTCCGCTCCACCGTCTCATCTCCACCCGACGAC	600
QY	671	GAGACTGTGACCAACGACGAAATTTGAGTGTGACCTCAAGGAGCATGTGATCAAGCGGTG	730
Db	601	GAGACGTCACCAACGACGAGATCGCGCGACCTCAAGGAGCAGCTCATCAAGCGGTG	660
QY	731	ATCCCGGAGAGTACCTTGTATGAGAGACATTTTCCACTTGAACCCCTCTGCGCGTTT	790
Db	661	ATCCCGGACAGTACCTGACGAGAGACATTTTCCACTTGAACCCCTCTGCGCGCTTC	720
QY	791	GTCAATGGAGGTCTCTCACGGTGTATGCTGTCTCACCGCGCGCAAGATCATCATGATCT	850
Db	721	GTCAATGGCGGGCCCAACGGGACCGCGGCTCACCGCGCGCAAGATCATCATGACAC	780
QY	851	TACGGAGATGGGGTCTCATGGTGTGTTGCTTCTCCGGGAAAGGATCCCAACGAGTT	910
Db	781	TACGGCGGATGGGGCGCGACGCGCGCGGCTTCTCCGGGCAAGGACCCGACCAAGTTC	840
QY	911	GATAGAGTGGTCTTACATTTGAGACAGGCTGTAAAGAGCATTTGTGCAAGTGCATTA	970
Db	841	GACCGGAGGGGCGCTTACATTCGCGAGGCGCGCAAGAGCATGTCGCCAGCGGCTTC	900
QY	971	GCCAGAAAGTGCAATTTGCAAGTGTCTTATGCAATGTTGTGTGCCCGGAGGCTTTGTCTGTC	1030

Db	901	GCCCGCGCTGCATCGTCGAGGTGTGTACGCCATCGCGTCCCGAGCCGCTCTCCGTCG	960
QY	1031	TTTGTGTGACCTATGCGACCGGGAAGATCCATGATAGGAGATTCTCAACATTTGTGAAG	1090
Db	961	TTCTGTGACTCTTACGGCACCAGGATCCCGACAGGAGATCCTCAAGATCGTCAAG	1020
QY	1091	GAGAACTTTGATTTTACGGCCCGGTATGATCTCTCACTCAACCTTGATCTCAAGAGGGTGG	1150
Db	1021	GAGAACTTCGATTTTACGGCCCGGATGATGATCAACCTCGACCTCAAGAGGGGCGG-	1079
QY	1151	AATAACAGGTTCTTGAAGACTGCTGCATATGACACACTTCGGCAGAGAGGCCCTGACTTC	1210
Db	1080	--CAACCGGTTTCAACAGACCGCGGCTACCGCCATTTCCGCCGCGAGATCCCGACTTC	1137
QY	1211	ACATGGGAGTGTGTCAGCCCTCAAGTGGGAGAGGCCCT	1250
Db	1138	ACATGGGAGTGTGTCAGCCGCTCAAGTATGAGAAGGCAT	1177

RESULT 14

AAC33674

ID AAC33674 standard; DNA; 1395 BP.

XX AC AAC33674;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.

XX KW Hybridisation assay; genetic mapping; gene expression control;  
XX KW protein identification; signal transduction pathway; metabolic pathway;  
XX KW promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 30-APR-1999; 99US-0132407P.

XX PR 04-MAY-1999; 99US-0132484P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 07-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

XX PR 19-MAY-1999; 99US-0134941P.

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XX PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
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PR 03-JUN-1999; 99US-0137528P.  
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PR 07-JUN-1999; 99US-0137724P.  
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PR 25-OCT-1999; 99US-0161406P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 52.8%; Score 783.6; DB 3; Length 1395;  
Best Local Similarity 79.7%; Pred. No. 3.6e-217;  
Matches 936; Conservative 1; Mismatches 235; Indels 2; Gaps 1;

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 139  
DB 100 GAGACTTTCCTATTACATCTCAGTCTGTGAACGAGGACACCCCTGACAAAGCTTTGCGAC 159  
QY 140 CAAATCTCCGATGCTGCTCGACGCTTCCCTTGACAGGACCCGACAGCAGAGTGGC 199  
DB 160 CAGATCTCTGATGCGAGTCTTGATGCTTCCCTTGACAGAGCCCTGATAGCAAGTTGCT 219  
QY 200 TCGAAACATGACCAAGACCAACTTGTGTCATGGTCTTCGAGAGATCACCAAGGCC 259  
DB 220 TGTGAGACATGCACCAAGACCAACATGGTTCATGGTTTTCGGTGAGATCACCAAGGCT 279  
QY 260 AAGCTTGATACGAGAAAGATCGTGGTGAACCTGCGAGAAATCGGCTTGTCTCAAC 319  
DB 280 ACGATTGATACGAGAAAGATTTGCGTGACACTTGGCTTCCATTGGATTCTCTGAC 339  
QY 320 GATGCGGACTGATGCTGACAACTGCAAGGTCTTGTAAACATTGACGAGCAGACCT 379  
DB 340 GATGTTGGTCTTGATGC--ACAAATGCAAAGTCTTGTAAACATTGAAACAGAGCCCA 397  
QY 380 GATATTGCCAGGGTGTGACGCGCCACCTTACCAAAAGACCCGAGGAATCGGTCTGA 439  
DB 398 GACATTGCTCAAGGTGTCAOAGTCACTTACCACCAAGTCCAGAGACATTTGAGCTGT 457  
QY 440 GACAGGGTCAATGTTGGCTATGCGACGAGAAACCCCGAGAAATGATGCAATTGAGT 499  
DB 458 GACCAAGGACATGTTTGGTATGCGACTGATGAACCCCTGAGCTCATGCTTTGAGT 517  
QY 500 CATGTTCTTGAACATAAATCGGTGCTGCTCACCGAGTTCGCAAGAACGGAACCTGC 559  
DB 518 CATGCTTGTGAACCAAGATTTGGTCTGCTCTCACTGAAGTCAGGAAGATGGAATGCT 577  
QY 560 CCATGTTGAGGCTGATGGGAAACCCAAAGTGAAGTGTGATTTACAATGCAACGGT 619  
DB 578 CGTTGTTAAGACCATGCGAAGACCCCAAGTCACTGTTGAGTACTTACAATGCAATGSC 637  
QY 620 GCAATGTTCCAGTTCGCTGCTCACACTGCTTATCTCCACCAATGATGAGACTGTG 679  
DB 638 GCTATGTTCCAGTTCGCTGCTCACACCCGCTCTGATCTCAACCCGACGATGAAACCGTT 697  
QY 680 ACCAAGCAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCGGAG 739  
DB 698 ACCAAGCAGATTCGCGGTGACCTCAAGGAGCATGTGATCAACCAATCATCCAGAG 757  
QY 740 AAGTACCTTGATGAGAAACCAATTTTCCAATTGAACCCCTCTGGCCGTTTGTCTCAATGA 799  
DB 758 AATATACCTTGACGACAAACCACTTTCCACCTCAACCCATCAGGCGGTTTGTGATCGG 817  
QY 800 GGTCTCAGCGTATGCTGCTCACCAGCCGACGATCATCATGATCTTACCGAGGA 859  
DB 818 GGACCAACACGGTATGCTGGTTTAACTGGACGCTAAGATCATCATTTGACATACGGAGA 877  
QY 860 TGGGGTGTCTCATGTTGGTGTGCTTCTCCGGAGGATCCCAACCAAGTTGATAGGAGT 919  
DB 878 TGGGGAGCTCATGGAGGTGGTGTCTTCTCAGGCAAGACCCCAACCAAGTGCACAGAGT 937  
QY 920 GTGCTTACATTTGAGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGATAGCCAGAGG 979  
DB 938 GGAGCTTACATCGTAGGCAAGCAGCAAGAGTGTGGTGGCTTAATGGCATGCTCGCAGG 997  
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTGTTGTCGCCGAGCCCTTGTCTCTTTTGTGAC 1039  
DB 998 GCTCTTGTCCAGTCTCATACGCCATTGGAGTACCCGAGCCCATTTGTCTCTKCGTTGAC 1057  
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAGGAGATTTCTCAACATTTGTGAAGAGAACTTT 1099

DB 1058 ACTTACGGAACAGGGTTGATTCAGACAGAGAGATCTGAAGATCGTGAAGAGACATTTC 1117  
QY 1100 GATTTACGGCCCGGTATGATCTCCATCAACCTTCAAGAGGGGTGGGAATAACAGG 1159  
DB 1118 GATTTACAGACCAGGAATGATGACAATCAACTTGGACTTTGAAGAGAGAGGAGAAATGGAAGG 1177  
QY 1160 TTCTTGAAGACTGCTGCATATGGACACTTTCGGCAGAGAGGACCCCTGACTTTCACATGGCAA 1219  
DB 1178 TTTGAGAAACCGGAGCGTATGSGACATTTTCGAAAGAGACGACCCCTGACTTTCACCTGGGAG 1237  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAG 1253  
DB 1238 GTGCTGAAGCCACTCAAGTGGGACAAACCTCAAG 1271

RESULT 15  
AAT99143  
ID AAT99143 standard; cDNA to mRNA; 1182 BP.  
XX AAT99143;  
XX 26-MAR-1998 (first entry)  
XX S-adenosylmethionine synthase 3 gene.  
XX S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;  
KW sam3; ss.  
XX Hordeum vulgare.  
XX JP09313186-A.  
XX 09-DEC-1997.  
XX 28-MAY-1996; 96JP-00133406.  
XX 28-MAY-1996; 96JP-00133406.  
XX (NIOC) NIPPON OIL CO LTD.  
XX WPI; 1998-080077/08.  
DR P-PSDB; AAW34542.  
XX S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil.  
PS Claim 6; Page 10-11; 13pp; Japanese.  
XX This sequence represents the S-adenosylmethionine synthase 3 (sam3) gene. This DNA sequence may be used in a vector to produce plants which are resistant to alkaline soil  
SQ Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 U; 0 Other;  
Query Match 52.4%; Score 778.6; DB 2; Length 1182;  
Best Local Similarity 79.2%; Pred. No. 9.3e-215;  
Matches 938; Conservative 0; Mismatches 244; Indels 3; Gaps 1;

QY 71 AAGATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAG 130  
DB 1 ATGGCGGCGGAGAGCGTCTCTTCAGTCCGAGTCCGTGAACGAGGGCCATCCCGACAAG 60  
QY 131 CTCTGCGACCAAAATCTCCGATGCTGCTCAACGCTTGCCTTGAACAGACCCAGACAGC 190  
DB 61 TTGTGTGACCAAGGTCTCCGACGCCGTCTTGACGCCCTGTTGGCCAGGATCTCTGACAGC 120  
QY 191 AAGGTTGCTCGGAAACATGCAACCAAGACCACTTGGTTCATGGTCTTCGAGAGATCACC 250  
DB 121 AAGGTTGCTCGGAGACCTGCAACCAAGACCAACATGTCATGGTCTTCGCGAGATCACC 180  
QY 251 ACCAAGGCCAACGTTGATCTACGAGAAGATCGTGGTGAACCTGCGAGAAACATCGGCTTC 310



Db 181 ACCAAGCCACCGTGGACTATGAGAAGATTGTGCGTGACACCTGCGCGACATTGGCTTC 240  
QY 311 GTCTCAAAACGATGTGGACTTGTATGCTGCAACTGCAAGTCTCTGTAAACATTGAGCAG 370  
Db 241 ATCTCTGACGACGTCGGTCTCGACGCGGACCATTTGCAAGGTGCTGTCACATCGAGCAA 300  
QY 371 CAGAGCCCTGATATGCCCAAGGTGTGCAAGGCCACCTTACCAAAAGACCCGAGGAAATC 430  
Db 301 CAATCCCTGACATTGCCCAGGGTGTTCATGGACACTTCAACAAAGGTCAGAGAGGTC 360  
QY 431 GGTGCTGGAGACGAGGGTCACATGTTTGGCTATGCCCGACGACGAAACCCAGAAATTGATG 490  
Db 361 GGCGCCGGTGACCAAGGTCATATGTTTGGCTATGCCACGGATGAGACCCCTGAGCTGATG 420  
QY 491 CCATTGAGTCATGTTCTTGCACAACTCAAACTCGGTGCTGCTCACCGAGGTTCGCAAGAAC 550  
Db 421 CCCCTCACCAACATGTTGGCACCAGCTCGAGCTCGCTCACCGAGGTTCGCAAGAAT 480  
QY 551 GGAACCTGCCCATGTTGAGGCTGATGGGAAACCCAAAGTGACTGTTGAGTATTACAAT 610  
Db 481 GGCACCTGTGCTGGCTGAGGCTGATGGAAAGACCCAGGTCAACATTGAGTACCTAAAT 540  
QY 611 GACAACGGTCCATGTTCCAGTTCGTGTGCCACACTGTGCTTATCTCCACCCAAATGAT 670  
Db 541 GAGGTTGGTCCCATGTTGCTGTTGTCGTCACACCGTCTCATCTCCACCCAGCATGAT 600  
QY 671 GAGACTGTGACCAACACGAAATTTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTG 730  
Db 601 GAGACCGTCACCAACATGAGATCGCCGGGACCTCAAGGAGCATGTATCAAGCCGGTG 660  
QY 731 ATCCCGGAGAGTACCTTGATGAGAAAGACCATTTTCCACTTGAACCCCTCTGGCCGTTTT 790  
Db 661 ATTCCCGGGAAGTATCTCGATGAACACCACTTCCACTTGAACCCGTCGGGTGCTTC 720  
QY 791 GTCAATTGGAGGTCTTCAAGGTGATGCTGTCTCACCGGCGGCAAGATCATCATGATCT 850  
Db 721 GTCATCGCGGGCCCTCATGGCGATGCGGTCTCACCGGCGCAAGATCATCATGACACC 780  
QY 851 TAGCGAGGATGGGTGCTCATGCTGTGTGCTTTCTCCGGGAAGGATCCCAACCAAGTT 910  
Db 781 TACGGTGGTGGGAGCCCATGGCGCGGCTTTCTCTGGCAAGGACCCGACCAAGGTC 840  
QY 911 GATAGGAGTGGTCTTACATTTGAGACAGGCTGTCTAAGAGCATTTGTGGCAAGTGGACTA 970  
Db 841 GACCGCAGTGGCGCTTACATTGCCAGGCAAGCGCCCAAGAGCATCATGCCAGCGGTCTC 900  
QY 971 GCCAGAGGTGCATTTGTGCAAGTGTCTTATGCCATTGGTGTGCCCGAGCCTTTGCTGTC 1030  
Db 901 GCACGCCGTGCATTTGTGAGATCTCATACGCAATCGGTGTACCTGAGCCTTTGTCTGTG 960  
QY 1031 TTTGTTGACACCTATGCGCACCGGAAGATCCCATGATAAGGAGATTCTCAACATTGTGAAG 1090  
Db 961 TTCGTGCTCTCTACCGGACCGGCAAGATCCCGGACAGGAGATCTCTAAGCTCGTGAAG 1020  
QY 1091 GAGAACTTTGATTTCAAGGCCGGTATGATCTCCATCAACCTTTGATCTCAAGAGGGGTGG 1150  
Db 1021 GAGAACTTTGACTTCAAGGCCGGGATGATCAGATTAACTTGATCTGAAGAAAGGTGG- 1079  
QY 1151 AATAACAGGTTCTTGAAGTCTGTGATATGGACATTCGGCAGAGAGGACCTGACTTC 1210  
Db 1080 --AAGAGGTTTCATCAAGACAGCTGTCTTATGGTCACTTTGGCGCGAGCATGCCGACTTC 1137  
QY 1211 ACATGGGAAGTGTCAAGCCCTCAAGTGGGAGAGGCCCTAAGGC 1255  
Db 1138 ACCTGGGAGGTGGTGAAGCCCTCAAGTTTCGACAGGCAATCTGCC 1182

Search completed: August 31, 2005, 01:31:36  
Job time : 819.183 secs

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**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1485	100.0	1485	4	US-09-424-978B-38	Sequence 38, Appl
2	866.8	58.4	1479	4	US-09-424-978B-40	Sequence 40, Appl
3	821.4	55.3	2183	4	US-09-424-978B-37	Sequence 37, Appl
4	819.6	55.2	1582	4	US-09-424-978B-35	Sequence 35, Appl
5	787.8	53.1	1353	4	US-09-424-978B-43	Sequence 43, Appl
6	777.8	52.4	1380	4	US-09-424-978B-41	Sequence 41, Appl
7	422.4	28.4	1283	4	US-09-949-016-4188	Sequence 4188, Ap
8	420.8	28.3	1283	3	US-09-318-448-22	Sequence 22, Appl
9	420.8	28.3	1283	4	US-09-023-655-1371	Sequence 1371, Ap
10	420.8	28.3	3495	4	US-09-976-594-470	Sequence 470, App
11	411.4	27.7	3320	4	US-09-949-016-1787	Sequence 1787, Ap
12	411.4	27.7	3328	3	US-09-318-448-20	Sequence 20, Appl
13	411.4	27.7	3328	4	US-09-949-016-68	Sequence 68, Appl
14	384.8	25.9	1173	4	US-09-948-796A-4152	Sequence 4152, Ap
15	306.8	20.7	1158	4	US-09-489-039A-4746	Sequence 4746, Ap
16	303.8	20.5	1206	4	US-09-252-991A-3328	Sequence 3328, Ap
17	303.8	20.5	1470	4	US-09-252-991A-3329	Sequence 3339, Ap
18	291.6	19.6	1208	2	US-08-403-852D-4	Sequence 4, Appli
19	291.6	19.6	1208	3	US-08-510-646B-4	Sequence 4, Appli
20	291.6	19.6	1208	3	US-09-231-818-4	Sequence 4, Appli
21	291.6	19.6	1208	4	US-09-635-359B-4	Sequence 4, Appli
22	291.6	19.6	5392	2	US-08-403-852D-1	Sequence 1, Appli
23	291.6	19.6	5392	3	US-08-510-646B-1	Sequence 1, Appli
24	291.6	19.6	5392	3	US-09-231-818-1	Sequence 1, Appli
25	291.6	19.6	5392	4	US-09-635-359B-1	Sequence 1, Appli
26	289.2	19.5	1164	4	US-09-543-681A-2958	Sequence 2958, Ap
27	284.2	19.1	17654	4	US-09-902-540-1161	Sequence 1161, Ap



600 AGTATTACATGACACAGCGTGCATGTTCCAGTTCGTGTCACACATGTCCTTATCTCCA 659  
643 AGTATAGCATGACAAATAGTGGTCCATGTTCCAAATAGGGTACACACTGTTCTTATCTCCA 702  
660 CCCAACATGATGAGACTGTGACCAACAGCAGAAATTCAGCTGACCTCAAGGAGCATGTGA 719  
703 CCCAACAGATGAGACGTTTACCAATGATGAGATGTCGCCGACCTTAAAGGAGCATGTGA 762  
720 TCAAGCGGTGATCCCGGAGAGTACCTTGATGAGAGAACCAATTTTCCACTTGAACCCCT 779  
763 TCAACACAGTATCCAGAGAGTACTTGTATGAGAACTACTATTTTCCACCTTAAACCAT 822  
780 CTGCGCGTTTGTCTATGAGAGTCTCAGCGTATGCTGCTCAACCGGCGGCAAGATCA 839  
823 CTGCGCGATTCGTTATTTGGTGGACCTCATGGTATGCTGCTCTCACTGGTCTGTAATAACA 882  
840 TCATCATATCTTACGGAGAGATGGGTGCTCATGGTGGTGGTCTTCTCCGGGAGGATC 899  
883 TCATCGACACTTATGGTGGTGGGTGCTCATGGTGGTGGTCTTCTCCGGGCAAGACC 942  
900 CCACCAAGGTGATAGAGTGGTCTTACATTTGAGACAGGCTGCTAAGAGCATTTGGG 959  
943 CAACCAAGTTCGACAGAGTGGTGCATACATTTGAAGGAGGCTGCAAGAGTATCGTAG 1002  
960 CAAGTGGACTAGCCAGAGGTGCATTTGTGCAAGTGTCTTATGCAATTTGGTGTCCCGAGC 1019  
1003 CTAGTGGACTTGTCTGTAGATGATCGTGCAGGTATCTTATGCAATCGGTGCTCGTGGC 1062  
1020 CTTTGTCTGTTTGTGACACCTATGGCACCGGGAAGATCCATGATAGGAGATCTCA 1079  
1063 CATTTGTCTGTTTGTGACACCTATGGCACTGGAAAGATCCCTGACAGGAAATTTTGA 1122  
1080 ACATTCGTAAGGAGAACTTTGATTTTCAGGCGCGTATGATCTCCATCAACCTTTGATCTCA 1139  
1123 AGATCTTGAAGGAACTTTGACTTCAGACCTGGAAATGATGCCATTAATCTTGGATTGA 1182  
1140 AGAGGGGTGGGAATAACAGGTTCTTGAAGACTGCTGATATGACATATGGACACTTCGGCAGAGAG 1199  
1183 AGAGGGGTGGCAATAAGAACTTTTGAAGAACTGCTGCTTATGGTCACTTTGGACGTGATG 1242  
1200 ACCCTGACTTCACATGGGAAGTGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATT 1259  
1243 ACCCCGATTTCAATGGGAAGTTGTCAAGCCCTCAAGTGGGAAAGGCCCAAGACTAAT 1302  
1260 CATTCACCTGCAATGCTGCGGAGTTTTTT 1289  
1303 AAGTGTCTCCCTATGTTTGTCTTTGTT 1332

## RESULT 3

US-09-424-978B-37

; Sequence 37, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 37

; LENGTH: 2183

; TYPE: DNA

; ORGANISM: Oryza sativa

US-09-424-978B-37

Query Match 55.3%; Score 821.4; DB 4; Length 2183;

Best Local Similarity 80.6%; Pred. No. 1e-244;

Matches 960; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 80 GAGACATTCCTTATTTACCTCAGAGTCAGTGAACAGGGGACACCTTGACAAAGCTCTGCGAC 139  
Db 800 GATACCTTCTCTTTACCTCGAGTCTGTGAACGAGGGCCACCTTGACAAAGCTCTGCGAC 859  
QY 140 CAAATCTCCGATGCTCTCGACCTTGCCTTGAACAGGAGCCGACAGCAAGGTGGC 199  
Db 860 CAAATCTCCGATGCTCTCGACCTTGCCTTGAACAGGAGCCGACAGCAAGGTGGC 919  
QY 200 TCGGAAAACATGACCAAGAACCAATTTGGTCTATGGTCTTCGGAGAGATCAACCAAGGCG 259  
Db 920 TGTGAGACTGACCAAGAACCAATTTGGTCTATGGTCTTCGGAGAGATCAACCAAGGCG 979  
QY 260 AACGTTGACTACGAGAAGATCGTGTGACACCTGACAGAAACATCGGCTTCGTCTCAAC 319  
Db 980 AACGTTGACTATGAGAAGATTTGTGAGAGACATCGCGTAAACATCGGCTTCGTCTCAAC 1039  
QY 320 GATGTGGGACTTGTGCTGACAACTGCAAGGCTCTTGTAAACATTTGAGCAGCAGAGCCCT 379  
Db 1040 GATGTGGGACTTGTGCTGACAACTGCAAGGCTCTTGTAAACATTTGAGCAGCAGAGCCCT 1099  
QY 380 GATATTTGCCAGGGTGTGACGGCCACCTTACCAAAAGACCCGAGAAATCGGTCTGGA 439  
Db 1100 GATATTTGCCAGGGTGTGACGGCCACCTTACCAAAAGACCCGAGAAATCGGTCTGGA 1159  
QY 440 GACCAAGGCTACATGTTTGGCTATGCCAGGAGAAACCCAGAAATTTGATGCCATTTAGT 499  
Db 1160 GACCAAGGACACATGTTTGGATATGCAACTGATGAGACCCCTGAGTGTGATGCCCCCTCAG 1219  
QY 500 CATGTTCTTGCAACTAACTCGTCTGCTCACCGAGGTTTGGCAAGAACCGAAGACCTGC 559  
Db 1220 CATGTTCTTGCAACTAACTCGTCTGCTCACCGAGGTTTGGCAAGAACCGAAGACCTGC 1279  
QY 560 CCATGTTTGGGCTGATGGGAAACCCAAAGTACTGTTGAGTATTACAAATGACAAAGCT 619  
Db 1280 GCATGGCTCAGGCTTGACGGGAAGACCCAAAGTACTGTTGAGTACCGCAATGAGAGCGT 1339  
QY 620 GCCATGGTTCAGTTCGTGTCACACTGCTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 1340 GCCATGGTTCGTGTCGTGTCACACTGCTGCTTATCTCCACCAACATGATGAGACTGTG 1399  
QY 680 ACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCCGTGTATCCCGGAG 739  
Db 1400 ACCAACGATGAGATTTGCTGCTGACCTGAAGGAGCATGTGATCAAGCCCTGTCAATCCCGAG 1459  
QY 740 AAGTACCTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCCGCTTGTCTATTGA 799  
Db 1460 CAGTACCTTGATGAGAAGCAATTTTCCACTTGAACCCCTCTGGCCGCTTGTCTATTGAG 1519  
QY 800 GGTCTCTCAGGCTGATGCTGCTCAACCGGCGCAGATCATCATCGTACTTTACCGAGGA 859  
Db 1520 GGACCTCATGCTGATGCTGCTCACTGCGCGGAGATCATCATTTGACACTTATGCTGCTG 1579  
QY 860 TGGGGTCTCATGCTGCTGCTTCTTCCCGGAGGATCCCAACAAAGTTGATAGGAGT 919  
Db 1580 TGGGGAGCTCAGGCTGCTGCTTCTTCTGCGAAGGACCCCAACCAAGTTGATGCTGCTG 1639  
QY 920 GGTGCTTACATTTGAGACAGCTGCTGAAGACATTTGCGCAAGTGTGAGTGTGATAGGAG 979  
Db 1640 GGAGCATACGTCGCAAGGCAAGCTGCCAAGAGCATTTGTTGCTAGTGGCTTGTCTGCCG 1699  
QY 980 TGCATTTGCAAGTGTCTTATGCCATTTGCTGCGCGAGCCCTTGTCTGCTTCTTGTCTGAC 1039  
Db 1700 TGCATTTGCAAGTGTCTTATGCCATTTGCTGCGCGAGCCCTTGTCTGCTTCTTGTCTGAC 1759  
QY 1040 ACCTATGGCACCGGAGAGATCCATGATGAAGGAGATTTCTCAACATTTGTGAAGGAGAACTTT 1099

Db 1760 ACATACGGCACTGGCAGGATCCCTGACAAAGGAGATCTCAAGATTGTGAAGGAGAACTTC 1819  
Qy 1100 GATTTACAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGATTAACAGG 1159  
Db 1820 GACTTACAGCCCTGGATGATCATCATCAACCTTGACCTCAAGAAAGGCGGCAACGGAGCG 1879  
Qy 1160 TTCTTGAAGACTGCTGATATGACACTTTCGGCAGAGAGACCTTGACTTTCACATGGGAA 1219  
Db 1880 TACCTCAAGACGGCGCTTACCGTCACTTCGGAAGGAGCAGCCAGACTTTCACCTGGGAG 1939  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATTTCATTCACACTGC 1270  
Db 1940 GTGGTGAAGCCCTCAAGTGGGAGAGCCTTCTGCTAAAGCTCCCTTTC 1990

## RESULT 4

US-09-424-978B-35

; Sequence 35, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1582

; TYPE: DNA

; ORGANISM: Zea mays

US-09-424-978B-35

Query Match 55.2%; Score 819.6; DB 4; Length 1582;  
Best Local Similarity 81.0%; Pred. No. 3e-244;  
Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
Qy 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACAGGGGACACCCCTGACAAAGCTCTGCGAC 139  
Db 152 GACACCTTCCTTCACTCGGAGTCTGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 211  
Qy 140 CAATCTCCGATGCTGCTCGACGCTTGCCTTGAACGAGGCCACGACGAGGCTTGGC 199  
Db 212 CAGGCTCAGATGCGCTTCTTGACGCTTGCCTTGTGAGGACCCCTGACAGCAAGGTTGCT 271

Qy 200 TGGAAACATGCACCAAGACCACTTGGTCTTCGAGAGATCAACCAAGGCC 259  
Db 272 TGTGAGACCTGCACCAAGACCAACATGCTCATGCTTGTGAGATCAACCAAGGCC 331  
Qy 260 AACGTTGACTACGAGAAGATCGTGCCTGACACCTGACGAAACATCGGCTTCGTTCAAC 319  
Db 332 NATGTGCACTACGAGAAGATTGTGAGGAGACCTGCGCAACATTTGGTTTGTGTCAAC 391  
Qy 320 GATGTGGACTTATGCTGACACTGCAAGTCTTGTAAACATTTGACGAGCAGGACCT 379  
Db 392 GATGTGCGGCTTGACCTGACCACTGACAGGTGCTCGTGAACATTTGACGAGTCCCT 451  
Qy 380 GATATTGCCAGGGTGTGACGCGCCACTTACCAAAAGACCCGAGGAAATCGGTGTGGA 439  
Db 452 GATATTGCTCAGGGTGTGATGCGCACTTACCAAGCGCCCGGAGAGATTGAGCTGTT 511  
Qy 440 GACCAAGGTCACATGTTTGGCTATGCGCAGGACGAAACCCCAAGATTGATGCAATGAT 499  
Db 512 GACCAGGGACACATGTTCCGGGTATGCGACCGATGAGACCCCTGAGTTGATGCTCCCTCAGC 571

Qy 500 CATGTTCTTTGCAACTAACTCGTGCTCGTCTCACGAGGTTTCGCAAGACGGAACCTGC 559  
Db 572 CATGTTCTTTGCCACCAAGCTAGGTGCTCGTCTCACGAGGTTCCGCAAGACGGAACCTGC 631  
Qy 560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTGAATGTTGAGTATTCAATGACAAACGTT 619  
Db 632 CCCTGGCTCAGGCTGATGGGAAAGACCCAGGTGACAGTCGAGTACCGCAATGAGGGTGGT 691  
Qy 620 GCCATGGTTCCAGTTCGTTGCTCCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 692 GCCATGGTCCCACTCCCGTGTCCACACCGTCTCATCTCCACCCAGCAGCAGACAGTGT 751  
Qy 680 ACCAACGACGAAATTTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739  
Db 752 ACCAATGATGATCGCTGCTGACTGAAGGAGCATGTTCATCAAGCCTATCATCCCTGAG 811  
Qy 740 AAGTACCTTGATGAGAGACCATTTTCCATTGTAACCCCTCTGGCCGTTTGTCTATTGGA 799  
Db 812 CAGTACCTTGACGAGAGACCATCTTCCACCTTAACCCATCCGGCCGCTTTGTCTATTGGT 871  
Qy 800 GGTCTCACGGTGTGCTGCTCACCGCGCGCAAGATCATCATCGACTTACCGAGGA 859  
Db 872 GGACCTCACGGGATGCTGGGCTCATCTGCGCGCAAGATCATCATTTGACACCTACGGTGGC 931  
Qy 860 TGGGTTGCTCATGTTGTTGTTGCTTCTCCGGGAGGATCCCAAGGTTGATAGGAGT 919  
Db 932 TGGGAGGCCATGGGTTGGCGCTTCTCCGGCAAGGACCCCAAGGTTGACCGCAGC 991  
Qy 920 GGTGTTTACATTTGAGACAGGCTGCTTAAGAGCATTTGGGCAAGTGGAGTACGACAGAGG 979  
Db 992 GGAGCCTATGTCGGGAGGAGGCTGCCAAGAGCATCTGTCGCGAGCGGCTTGTCTCGCGC 1051  
Qy 980 TGCATTGTGCAAGTGTCTTATGCCATTGTTGCCCGAGCCTTGTCTGTCTTGTCTGAC 1039  
Db 1052 GCCATGCTCCAGGTGCTCTACGCCATCGCGGTGCCCGAGCCTCTCTCGTGTCTGAC 1111  
Qy 1040 ACCTATGACCGCGGAGATCATGATGAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099  
Db 1112 ACGTACGGCACGGCGCATCCCCGACAGGAGATCCTCAAGATTGTCAAGGAGAACTTC 1171  
Qy 1100 GATTTACGGCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGATTAACAGG 1159  
Db 1172 GATTTACGGCCTGGCATGATTATCATCAACCTTGAACCTCAAGAAAGCGGCAACGGGCGC 1231  
Qy 1160 TTCTTGAAGACTGCTGCATATGGACACTTCGCGAGAGAGCCCTGACTTTCATATGGGAA 1219  
Db 1232 TACCTCAAGACGGAGCCTACGGCCACTTCGGAAGGAGACCCCTGACTTTCACCTGGGAG 1291  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCCCTAAGGCCA 1257  
Db 1292 GTGGTGAAGCCACTCAAGTCGGAGAAACCTTCTGCCTA 1329

## RESULT 5

US-09-424-978B-43

; Sequence 43, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 43
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-424-978B-43

Query Match      53.1%; Score 787.8; DB 4; Length 1353;
Best Local Similarity 77.8%; Pred. No. 2.2e-234;
Matches 964; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

QY 71 AAGATGCGCAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACACCTCGACAAG 130
DB 55 ATGCGCGCGAGAGCTTCCTTCACGTCGAGTTCGTGAACGAGGCGCATCCGACAG 114

QY 131 CTCGCGACCAAAATCTCCGATGCTCTCTCGAGCTTGCCTTGAACAGGACCCAGACAGC 190
DB 115 CTGTGCGACCAAGTCTCTGACGCGCTCTTGACGCGCTGCTTGGCCCGAGGATCCTGACAGC 174

QY 191 AAGTTTCCCTGCGAAACATGCAACAGACCAACTTGGTCATGCTCTCGAGAGATCACC 250
DB 175 AAGTTTCTTGGCAGACCTGCAACAGACCAACATGGTCATGGTCTTTCGCGAGATCACC 234

QY 251 ACCAAGGCCAACTGCTGACTACGAGAAGATCGTGGTGACACCTGCGAGAACATCGGCTTC 310
DB 235 ACCAAGGCCAACCTGACTATGAGAAGATGTGCGCGACACCTGCGTGACATCGGCTTC 294

QY 311 GTCTCAACGAGTGGGACTTGATGCTGACAACTGCAAGSTCCTTGTAAACATTTGACAG 370
DB 295 ATCTCTGACGACGTGCTCGATGCGGACCACTTGCAAGGTGCTCGTCAACATCGAGAG 354

QY 371 CAGAGCCCTGATATTGCGCAGGCTGTGACGGCCACTTACCAAAAGACCCGAGGAAATC 430
DB 355 CAATCCCTGACATTTGCCAGGGTGTTCAGCGACACTTCAACAAAGGCTCCAGAAGAGGTC 414

QY 431 GGTGCTGGAACAGAGGTCACTGTTTGGTGTGCTGACGAGCAAGCAACCCAGAAATGAG 490
DB 415 GGGCGCGGTGACAGGGCATCATGTTTGGCTGCGCACTGATGAGACCTTGAGCTGATG 474

QY 491 CCATTGAGTCATGTTCTTGCAACTAAACTCGGTGCTCGTCTCACCGAGGTTGCCAAGAAC 550
DB 475 CCCTCACCACATGCTTGGCACCAGCTCGGAGCTCGCTCACCGAGTCCGCAAGAT 534

QY 551 GGAACCTGCCATGTTGAGGCTGATGGGAAACCCAAAGTGACTGTTGAGTATTAAT 610
DB 535 GGCACCTGCGCTGCTGAGGCTGATGGAAAGACCCAGGTCACTTGAATGATCTAAAC 594

QY 611 GACAAAGGTGCAATGTTCCAGTTCGTGTGCTGCTGACACTGCTTATCTCCACCCAAATGAT 670
DB 595 GAGGTTGGTCCATGTTGCGGTTGCTGTGTGCTGACACCGTCTCTATCTCCACCCAGCATGAT 654

QY 671 GAGACTGTGACCAACGACGAAATTTGACGCTGACCTCAAGGAGCATGTGATCAAGCGGTG 730
DB 655 GAGACGTCACCAACGATGAGATCGTGCAGACCTCAAGGAGCATGTGATCAAGCGGTG 714

QY 731 ATCCCGGAGAAGTACCTTGATGAGAAGACATTTTCCATTGAAACCCCTCTGCGCGCTTTT 790
DB 715 ATTCGCGGAAGTACCTCGATGAGAACACCATCTTCCACTGAAACCATCGGCGCGCTTT 774

QY 791 GTCATTTGAGGTCTCACCGTGTGCTGCTCTCACCGCGCGCAAGATCATATCGATCT 850
DB 775 GTCATCGGTGGCCCTCACGCGATGCGGTCTCACCGCGCGCAAGATCATATCGACACC 834

QY 851 TAGCGAGGATGGGGTGTCTCATGTTGTTGTTGCTTTCTCCGGGAAGGATCCACCAAGTTT 910
DB 835 TATGTTGGTGGGGACCCACGCGCGGTGCTTCTCTGGCAAGGACCCCTACCAAGTTC 894

QY 911 GATAGAGTGGTCTTACATTTGAGACAGGCTGTGTAAGACATTTGGCAAGTGAAGTGA 970
DB 895 GACCGCAGTGGCGCTTACATTTGACGAGGCTGCAAGAGCATCATCGCAGCGGCTTC 954

QY 971 GCCAGAGGTGATTTGCAAGTGTCTTATGCAATGTTGTGCCCGAGCTTTGCTGTGTC 1030
DB 955 GCACGCGGTGATTTGTGAGATCTCATATGCAATCGGTGTACCTGAGCGCTTTGTGTGTG 1014
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## RESULT 6

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US-09-424-978B-41
; Sequence 41, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Triticum aestiva
US-09-424-978B-41
```

```
Query Match      52.4%; Score 777.8; DB 4; Length 1380;
Best Local Similarity 79.0%; Pred. No. 2.9e-231;
Matches 933; Conservative 4; Mismatches 241; Indels 3; Gaps 1;

QY 77 GCAGAGACATTCCTATTTTACCTCAGAGTCAGTGAACGAGGACACCTGACAGCTCTGC 136
DB 79 GCGGAGAGCTTCCTTTCACGTCGAGTCTGTGAACGAGGCGCATCCGACAGCTCTGT 138

QY 137 GACCAAAATCTCGAGTGTCTCTCGACGCTTCCCTTGAAACAGGACCCAGACAGCAAGTT 196
DB 139 GACCAAGTCTCGAGCGCTCTTGGATGCTCTTGGCCAGGATGCGCAGCAGAGTTC 198

QY 197 GCTCGGAAAATGCAACCAAGACCAATTTGGTTCATGTTCTTCGAGAGATCAACCAAG 256
DB 199 GCTCGGAGACCGTCAACCAAGACCAATGTTGTCATGTTCTTGGGCGAGATCAACCAAG 258

QY 257 GCCAAGTGTGATGAGAGATCGGTGACACCTGCGAGGACATCGGCTTCGTCCTCA 316
DB 259 GCCACCGTCGATGAGAGATCGGTGTCACCTGCGCAACATCGGTTTCATCTCT 318

QY 317 AACGATTTGGGACTTGTGTCGACAACTGCAAGGCTCTTGTAAACATTTGAGCAGCAGAGC 376
DB 319 GATGAGTGTGTCGACGCCGACCGTGTGCAAGTGTCTGTCACATCGAGCAGCAGTCC 378

QY 377 CCTGATATTGCGCGAGGTTGTGCAACGCGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCT 436
```







/ FILING DATE: HEREWITH  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Zeller, Karen J.  
/ REGISTRATION NUMBER: 37,071  
/ REFERENCE/DOCKET NUMBER: PA-0001 US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (650) 855-0555  
/ TELEFAX: (650) 845-4166  
/ INFORMATION FOR SEQ ID NO: 1371:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1283 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ IMMEDIATE SOURCE:  
/ LIBRARY: GENBANK  
/ CLONE: G36326  
/ US-09-023-655-1371

Query Match 28.3%; Score 420.8; DB 4; Length 1283;  
Best Local Similarity 62.4%; Pred. No. 4.4e-120;  
Matches 700; Conservative 0; Mismatches 407; Indels 15; Gaps 2;

QY 76 GGAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGTCTG 135  
DB 107 GGAGGACATTCCTTTTACCTCAGAGTCGCTCGGGGAAAGGCCACCCAGATAAAGATTG 166

QY 136 CGACCAAACTCCGATGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGT 195  
DB 167 TGACCAAACTCAGTATGCTGCTTGTATGCCACCTTCAGCAGGATCTCGTATGCCAAAAGT 226

QY 196 TGCCTCGAAAACATGCACCAAGCAAACTTGTGTCATGCTTTCGAGAGATCACCACCAA 255  
DB 227 AGCTTGTGAACCTGTGTAAACTGGAATGATCTTCTGCTGGGAAATTAATCATCCAG 286

QY 256 GGCAACAGTTGACTACGAGAAAGATCGTGCCTGACACCTGCGAGAACTCGGCTCGTCTC 315  
DB 287 AGCTGCTGTGACTACGAGAAAGTGGTTCGTAAGCTGTAAACACATTTGGATATGATGA 346

QY 316 AAACAGATGGGACTGTGTCAGACACTGCAAGTCTTGTAAACATTTGACGACAGAG 375  
DB 347 TTCTTCCAAAGTTTGTACTCAAGACTTTGTAACGCTGTGTGCTTGGAGCAACATC 406

QY 376 CCTGATATTGCCAGGGTGTGCACGGCCACCTTACCAAGACCCGAGGAAATCGGTGC 435  
DB 407 ACCAGTATTGCTCAAGTGT-----TCATCTTGACAGAAATGAAGAGACATTTGGTGC 460

QY 436 TGGAGACAGGTTCATATTTTGGCTATGCCAGGACGAAACCCAGAAATGATGCCATT 495  
DB 461 TGGAGACAGGGCTTAATTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCCCTT 520

QY 496 GAGTCATGTTCTGCACTAAACTCGGTCTCGTCTCACCGAGGTTGCGAAGAACGGAC 555  
DB 521 AACCATTTCTTGGCACACAAGCTAAATGCCAAACTGCGAGAACTACCGCTAATGGCAC 580

QY 556 CTGCCCATGTTGAGGCTGTGGGAAACCCCAAGTGTGTTGAGTATTACAATGACAA 615  
DB 581 TTTGCTTGTACGCCCTGATCTTAAAACTCAAGTTACTGTGAGTATATGCAAGATCG 640

QY 616 CGGTGCCATTTGTTCCAGTTTGTGTCCACATGTGTTTATCTCCACCCCAACATGATGAGAC 675  
DB 641 AGGTGCTGTCTCCCATCAGAGTCCACAATTTGTTATCTGTTGACGATGATGAAGA 700

QY 676 TGTGACCAACGAGAAATTTGAGCTGACCTCAAGAGCATGTGATCAAGCCGCTGATCCC 735  
DB 701 GGTTTGTCTGTGATGAAATGAGGATGCCCCCTAAAGAGAAAGTCATCAAGCAGATTGTGCC 760

QY 736 GGAGAAAGTACCTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGCGCCGTTTGTGAT 795

DB 761 TGCAGAAATACCTTGATGAGGATACAACTACCACTCAGCCAAAGTGGCAGATTGTTAT 820  
QY 796 TGGAGGTCTCACCAGTATGCTGTCTCACCGCCGCAAGATCATCATCTGACTTACGG 855  
DB 821 TGGTGGGCTCAGGGTATGCTGCTTTGACTGGACGGAAATCATTTGTGGACACTTATGG 880  
QY 856 AGGATGGGGTCTCATGTTGGTGTGCTTTCTCCGGGAAGGATCCCAAGGTTGATAG 915  
DB 881 CGGTTGGGTGCTCATGAGAGGAGTGCCTTTTCAGGAAAGGATTTATCAAGGTCGACCG 940  
QY 916 GAGTGGTCTTACATTTGTGACACAGGCTGTCTAAGAGCATTTGTGCAAGTGGACTAGCCAG 975  
DB 941 TTCAGCTGCTTATGCTGCTGCTGGTGGCAAAATCCCTGTTAAAGAGGCTGTGCGG 1000  
QY 976 AAGTGCATTTGTGCAAGTGTCTTATGCAATTTGGTGTGCGCCGAGCTTTGTCTCTTTGT 1035  
DB 1001 GAGGGTTCTTGTTCAGGTCTCTTATGCTATTTGGAGTTTCTCATCAATTTATCTCCAT 1060  
QY 1036 TGACACCTATGGCACCGGAGATCCATGATAAGAGATTTCTCAACATTTGTGAAGGAGAA 1095  
DB 1061 TTTCCATTTATGTTACCTCTCAGAAAGTGAAGAGAGCTATTAGAGATTGTGAAGAGAA 1120  
QY 1096 CTTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGTGATCTCAAGAGGGTGGGAATAA 1155  
DB 1121 TTTGCAATCTCGCCCTGGGTCATTGTGAGGATCTGGATCTGAAGAAGCCCAATTTATCA 1180  
QY 1156 CAGGTTCTTGAAGACTGCTGCATATGACACATTTGCGGAGAGA 1197  
DB 1181 -----GAGGACTGCGAGCTATGGCCACTTTGGTAGGGA 1213

RESULT 10  
US-09-976-594-470  
; Sequence 470, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 470  
; LENGTH: 3495  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673549 2600262CB1  
; NAME/KEY: unsure  
; LOCATION: 2831-2993  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-976-594-470

Query Match 28.3%; Score 420.8; DB 4; Length 3495;  
Best Local Similarity 62.4%; Pred. No. 9.1e-120;  
Matches 700; Conservative 0; Mismatches 407; Indels 15; Gaps 2;

QY 76 GGCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGTCTG 135  
DB 156 GGAGGGCACATTCCTTTTACCTCAGAGTCGCTCGGGGAAAGGCCACCCAGATAAAGATTG 215

QY 136 CGACCAAACTCCGATGCTGCTCGACGCTTGTGAAACAGGACCCAGACACCAAGGT 195  
DB 216 TGACCAAACTCAGTATGCTGCTTGTATGCCCCATTCAGCAGGATCTGTATGCCAAGT 275

QY 196 TGCTCGGAAACATGCACCAAGACCAACTTGGTTCATGCTTTCGGAGAGATCACCACCA 255

Db 276 AGCTTGAAACTGTTGCTAAAACTGGAATGATCCTCTTGTGCTGGGAAATTACATCCAG 335  
Qy 256 GCGCAACGTTGACTACGAGAAGATCGTGGGTGACACCTCGCAGGAACATCGGCTTCGTC 315  
Db 336 AGCTGCTGTTGACTACGAGAAGTGGTTCGTGAAGCTGTTAAACATTTGGATATGATCA 395  
Qy 316 AAACGATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAG 375  
Db 396 TTCTTCCAAAGGTTTGAAGTACAAAGCTTGTAACTGCTGGTAGCCCTTGGAGCAACAGTC 455  
Qy 376 CCTCGATATTGCCAGGCTGTGCACGCCCACTTACCAAAAGACCCGAGGAATCGGTC 435  
Db 456 ACCAGATATTGCTCAAGGTG-----TCATCTTGACAGAAATGAAGAAGACATTGGTC 509  
Qy 436 TGAGACCAAGGTCACATGTTTGGCTATGCCAGGAGAAACCCAGAAATTGATGCCATT 495  
Db 510 TGGAGACCAAGGCTTAATGTTTGGCTATGCCACTGATGAACCTGAGGAGTGTATGCCATT 569  
Qy 496 GAGTCATGTTTGCACAACTAAACTCGGTGCTGCTCAACGAGGTTTGCAGAAAGCAAC 555  
Db 570 AACCATTTGCTTGGCACAAAGCTAAATGCCAACTGGCAGAACTACGCCGTAATGGCAC 629  
Qy 556 CTGCCCATGTTGAGCGCTGATGGGAAACCCCAAGTGAAGTGTGATATTACAAACAA 615  
Db 630 TTGCTTGGTTACGCCCTGATTTCTAAAACTCAAGTTACTGTGCGATATATGACGATCG 689  
Qy 616 CGGTGTCATGTTTCCAGTTTCTGCTCACACCTGCTTATCTCCACCAACATGATGAGAC 675  
Db 690 AGGTGCTGCTTCCATCAGAGTCCACAAATTTTATATCTGTTACGATGATGAAGA 749  
Qy 676 TGTGACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGATGCC 735  
Db 750 GGTGTTGCTTGTGAAATGAGGATGCCCTTAAAGGAGAAAGTCAATCAAGACGATTTGTGC 809  
Qy 736 GGAGAGTACCTTGATGAGAGAACCAATTTCCATTTGAACCCCTCTGGCCGTTTGTAT 795  
Db 810 TCGGAAATACCTTGATGAGGATACAATCTACCACCTACAGCCAAAGTGGCAGATTTGTTAT 869  
Qy 796 TGGAGTCTCTACGGTGATGCTGCTCTACCGGCCCAAGATCATCATGATACTTACCG 855  
Db 870 TGGTGGCCCTCAGGTTGATGCTGTTTGAAGTGGACGGAATAATCTGTTGACACTTATGG 929  
Qy 856 AGATGGGTGCTCATGTTGGTGGTCTTTCTCCGGAAAGGATCCCAAGGTTGATAG 915  
Db 930 CGGTGGGTGCTCATGAGGAGGTGCCCTTTTCAAGGAAAGGATATATCAAGGTGACCG 989  
Qy 916 GAGTGTGCTTACATTTGACAGACGCTCTAAGACATTTGGCAGTGGAGTGGATAGCCAG 975  
Db 990 TTCAGTCTTATGCTGCTGCTTGGGTGGCAAAATCCCTTGTAAAGGAGGTCTGTGCG 1049  
Qy 976 AAGGTGCAATTGTGCAAGTGTCTTATGCCATTGTTGTCGCGAGCCCTTGTCTGCTTTGT 1035  
Db 1050 GAGGTTCTTGTTCAGTCTCTTATGCTATTTGAGTTTCTCATCCATATCTATCTCCAT 1109  
Qy 1036 TGACACCTATGGCACCGGAAAGATCCATGATAGGAGATTTCTCAACATTTGCAAGAGAA 1095  
Db 1110 TTTCCATTTATGTTACCTCTCAGAAAGTGAAGAGAGCTATTAGAGATTTGCAAGAGAA 1169  
Qy 1096 CTTTGTATTTAGCCCGGCTATGATCTCCATCAACCTTGTATCTCAGAGGGGTGGGAATA 1155  
Db 1170 TTTTCATCTCCGCTTGGGGTCAATTTGTCAGGGATCTGGATCTGAAAGAACCAATTATCA 1229  
Qy 1156 CAGGTTCTTGAAGACTGCTGATATGACACTTTCCGACAGAA 1197  
Db 1230 -----GAGACTGACGCTATGACCACCTTTGTAGGGA 1262

## RESULT 11

US-09-949-016-1787  
; Sequence 1787, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1787  
; LENGTH: 3220  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1787

Query Match 27.7%; Score 411.4; DB 4; Length 3220;

Best Local Similarity 62.5%; Pred. No. 7,3e-117;

Matches 662; Conservative 0; Mismatches 391; Indels 6; Gaps 1;

Qy 86 TTCCTATTTCCTCAGAGTCAGTGAACGAGGGACACCTCTGACAAGCTCTGCGACCAATC 145  
Db 123 TTCTATGTTTTCATATCGAGTCTGTGGGAGAGGACACCCGGATTAAGATCTGTGACCATC 182  
Qy 146 TCCGATGCTGCTCGACGCTTTCGAAACAGGACCCAGACAGCAAGGTTCCCTGCGAA 205  
Db 183 AGTGATGAGTGTGATGCTGATGCTTCAAGCAAGACCCCAATGCGAAGTGGCTGTGAG 242  
Qy 206 ACATGCAACCAAGACCAACTTGTCTCATGCTTTCGGAGAGATCACCAAGGCCAACGTT 265  
Db 243 ACAGTGTGCAAGACCGGCATGCTGCTGTGTGTGAGATCACCTCAATGSCCATGGTG 302  
Qy 266 GACTACGAGAGATCGTGGTGACACCTGCGAGGAACATCGGCTTCGTCTCAAAACGATGTG 325  
Db 303 GACTACCAAGCGGTGTGAGGGACACCATCAAGCAACATCGGCTACGATGACTCAGCCCAAG 362  
Qy 326 GGACTTGATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAGACCCCTGATATT 385  
Db 363 GCTTTGACTTCAAGACTTGTGCAACGCTGCTGTGGCTTTTGGAGCAGCAATCCCGACATATT 422  
Qy 386 GCCCAGGTTGTCACGCGCCACCTTACAAAAAGACCCGAGGAAATCGGTGCTGGAGACCAAG 445  
Db 423 GCCCAGTG-----CGTCCATCTGGACAGAAATGAGGAGGATGTGGGGCAGAGATCAG 476  
Qy 446 GGTCACTGTTTGGCTATGCGACGACCAACCCAGAAATTTGATGCCATTGATGATCATGTT 505  
Db 477 GGTGTTGATGTTTGGCTATGCTTACCGACGAGACAGAGGAGTGCATGCCCTTCAACCATC 536  
Qy 506 CTTCGCAACTAAACTCGGTGCTGCTCTACCGAGGTTTCGCAAGACGGAACCTGCCCATGG 565  
Db 537 CTTCGCTCAAGCTCAACGCCGGATGCGACCTCAGCGGCTCCGGCTCTCCCTCTGG 596  
Qy 566 TTGAGGCTGATGGGAAACCCCAAGTGAAGTGTGAGTATTACAAATGACAAACGGTGCCTATG 625  
Db 597 CTGGGCTGACTCTTAAGACTCAGGTGACAGTTCAGTACATGTCAGGACAAATGGCGCAGTC 656  
Qy 626 GTTCAGTTCGTGTCACACTGTGTTATCTCCACCCCAACATGATGAGACTGTGACCAAC 685  
Db 657 ATCCCTGTGCGCATCCACCATCTGTCATCTCTGTGACGACCAACGAAAGACATCACGCTG 716  
Qy 686 GACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGCATCCCGAGAGATAC 745  
Db 717 GAGGAGATGCGAGGCGCTTGAAGGCAAGTTCATCAGGCGCTGGTGGCGGCCAAGTAC 776  
Qy 746 CTTGATGAGAGAACCAATTTTCCATTGAACCCCTCTGGCCGCTTTTGTCTCAATTTGAGGCTCT 805  
Db 777 CTGGACGAAGACACCGCTCTACACCTGCGAGCCCGCTGGGCGCTTTGTTCATCGAGGTC 836  
Qy 806 CACGCTGATGCTGTTCTCACCGCGCGGAAGATCATCATCATCTTACGAGGATGGGT 865



Best Local Similarity 62.5%; Pred. No. 7.3e-117; Matches 662; Conservative 0; Mismatches 391; Indels 6; Gaps 1;	
QY	86 TTCTTATTTACCTCAGATCAGTGAACGAGGGACACCTGACAAAGCTCTGCGACCAATC 145
Db	123 TTCTATGTTACATCGGAGTCTGTTGGAGAGGACACCCGGATAAGATTTGTGACCAATC 182
QY	146 TCCGATGCTGTCTCGACGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGCTCGGAA 205
Db	183 AGTGATGCACTGTGGATGCCATCTCAAGCAAGACCCCAATGCCAAGTGGCTGTGAG 242
QY	206 ACATGACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCAACCAAGGCCACAGTT 265
Db	243 ACAGTGTCAAGACCCGGCATGGTGTCTGTGTGTGAGATCACTCAATGGCCATGGTG 302
QY	266 GACTACGAGAAGATCGTGGTGACCTCGCAGCAACATCGGCTTCGTCTCAACAGATGG 325
Db	303 GACTACAGCGGTGTGAGGAGACATCAAGCACAATCGCTACGATGACTCAGCCAAG 362
QY	326 GGAATTGATGCTGACAACTGCAAGGTCCTTTGTAACATTTGAGCAGAGACCCCTGATAT 385
Db	363 GGCTTTGACTTCAAGACTTGCACAGTGTCTGTGGCTTTGGAGCAGCAATCCCAGATAT 422
QY	386 GCCAGGGTGTGACGGCCACCTTACAAAGACCCGAGGAATCGGTGTGAGACCAAG 445
Db	423 GCCCAGTG-----CGTCCATCTGGACAGAAATGAGGAGGATGTGGGGCAGGAGATCAG 476
QY	446 GGTTCATGTTTGGCTATGCCAGGACGAAACCCAGAAATGATGCAATGTGATGATGTT 505
Db	477 GGTGTTGATGTTTGGCTATGCTACCGACGAGACAGAGGATGTCCTCCCTCACCATCATC 536
QY	506 CTTGCAACTAAACTCGGTGTCTGTCTCAGCGAGTTTCGAAAGAACCGAACCTGCCCATGG 565
Db	537 CTTGCTCACAAGCTCAACGCCGGATGGCAGACCTCAGGGCTCCGGCTCTCCCTCGG 596
QY	566 TTGAGCCTGATGGGAAAACCAAGTACGTGTTGAGTATTAATGAACAAAGGTGCCATG 625
Db	597 CTGCGGCTGACTCTAAGACTCAGGTGACAGTTTCACTATGACGAGCAATGCGCGAGTC 656
QY	626 GTTCCAGTTTGTGTGCACACTGTCTTATCTCCACCCCAACATGATGAGACTGTGACCAAC 685
Db	657 ATCCCTGTGGGATCCACACCACTGCTCATCTCTGTGCGACACAAAGACATCAGCTG 716
QY	686 GAGCAATTCGACCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAGAGTAC 745
Db	717 GAGGATGCGCAGGCGCTGAAGGAGCAAGTCACTCAGGGCCGTGTGCGCGCCAGTAC 776
QY	746 CTTGATGAGAAGACCAATTTTCCACTTGAAACCCCTCTGGCCGTTTGTCTATTTGAGGTCT 805
Db	777 CTGGACGAAGACACCGTCTACCACTGCAGCCAGTGGCGGTTTGTCTATCGGAGTCCC 836
QY	806 CAGGTTGATGCTGTCTCAGCGCCGCAAGATCATCATCGATCTTACGAGGATGGGT 865
Db	837 CAGGGGATGCGGGTGTCACTGGCCGTAAAGATTTTGTGACACCTATGGCGGCTGGGG 896
QY	866 GCTCATGGTGGTGTCTTTCTCCGGAAGGATCCCAAGGTTTATAGGAGTGTGTCT 925
Db	897 GCTCATGGTGGTGGGCTTCTCTGGGAAGGACTACACCAAGGTAGACCGCTCAGCTGCA 956
QY	926 TACATTTGTGAGACAGGCTGTGAAGCATTTGTGGCAAGTGGATAGCCAGAGAGGTGCAT 985
Db	957 TATGCTGCCGCTGGGTGGCCAAAGTCTCTGGTGAAGCAGGGCTCTGCGCGAGAGTGCCT 1016
QY	986 GTGCAAGTGTCTATGCCATTTGGTGGCCGAGCTTTGTCTGTCTTTGTGACACCTAT 1045
Db	1017 GTCAGGTTTCTTATGCCATTTGTGTGGCGAGCGCTGTCCATTTTCCATCTTCACTTAC 1076
QY	1046 GGCACCGGAAGATCCATGATAGGAGATTTCTCAATTTGTGAAGGAGAACTTTGATTTTC 1105
Db	1077 GGNACCTCTCAGAAGACAGCGAGAGCTGCTGGATGTGTGATGAAGAACTTCGACCTC 1136
QY	1106 AGCCCGGTATGATCTCCATCAACCTTTGATCTCAAGAGG 1144

Db 1137 CGGCCGGCGTCAATGTCTCAGGATTTGGCAATTTGAAGAAG 1175

RESULT 14  
US-09-248-796A-4152  
; Sequence 4152, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 4152  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Candida albicans  
; US-09-248-796A-4152

Query Match 25.9%; Score 384.8; DB 4; Length 1173; Best Local Similarity 61.0%; Pred. No. 6.8e-109; Matches 645; Conservative 0; Mismatches 407; Indels 6; Gaps 1;	
QY	80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC 139
Db	31 GAAACTTTCTCTTTTCACTTTCAGATCCGTTGGTGAAGGTCAACCAGATAAGATTTGTGAC 90
QY	140 CAAATCTCCGATGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199
Db	91 CAACTCTCCGATGCCATTTAGTCTGTTTGTAGTCTTGTGATTCATTTGTCAAAGTTGCT 150
QY	200 TCGCAAAACATGACCAAGACCAACCTTGGTCATGCTTTCGGAGAGATCAACCAAGGCC 259
Db	151 TGTGAACCTGCTGCCAAAACCGGTATGATTTGTTTGGTGAATTTACCACTAAAGCT 210
QY	260 AACGTTGATGACGAGAAGATCGTGTGACACCTGACAGGAAACATCGGCTTCTCTCAAC 319
Db	211 CAAATGGATTTATCAAAAAATCATTAGAGACACCATTAACACATTTGGTTACGACGATTC 270
QY	320 GATGTGGGACTTGTGCTGACAACTGCAAGGTCCTTTGTAACATTTGAGCAGCAGAGCCCT 379
Db	271 GAAAAGGTTTGTATTACAGACTTGTAAACGCTCTTGGTTGCATTTGAACAACATCTCCA 330
QY	380 GATATTGCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
Db	331 GATATTGCTCAAGGTTTACATTTACGA-----AAAAGCTTTTGAAGAGTTGGGTGCTGCT 384
QY	440 GACCAAGGTACATGTTTGGCTATGCCAGGAGCAAAACCCAGAAATTTGATGCAATGAGT 499
Db	385 GATCAAGGTATTATGTTTGGTTATGCCACCGATGAACCCGATGAAAAATTTGCCATTTGACC 444
QY	500 CATGTTCTTGCAACTAAACTCGTCTCTCACCGAGTTTCGCAAGAACGGAACCTTGC 559
Db	445 ATTTATTGGCCCACAAAATTTGAATGCTGCTTGGCTTCTGCCAAGATCAGGTTCTCTTG 504
QY	560 CCATGTTTGAGGCTGTATGGGAAAAACCAAGTGACTGTTGAGTATTTACAAATCAACAGCT 619
Db	505 CCATGTTTGAGACCAAGATACCAAAACCAAGTCAACCATCGAGTATGAAAAGATGCTGCT 564
QY	620 GCCATGTTTCCAGTTTGTGTGTCACACTGTGTTATCTCCACCAACATGATGAGACTGTG 679
Db	565 GCAGTTATCCCAAAAAGAGTGCACAAATTTGTTATTTCCACTCAACATGCGCCGAGAAATC 624
QY	680 ACCACGACGAAATTTGACGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGAG 739
Db	625 ACCACCGAAATTTGAGAAAAAATAATTTGAACATATCATCAAGCAAGATCATCCAGAA 684

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QY 740 AAGTACCTTGTGAGAGACCAATTTTCCACTTGAACCCCTCGGCCGTTTGTCTATTGA 799
Db 685 CATTTATTAGACGACAAAATCTATCTACCAATTCAGCCATCAGGAGATTCGTCAATGGT 744
QY 800 GGTCTCTACGGTGTGCTGGTCTCACCGGCCGCAAGATCATCATCGATCTTACGGAGA 859
Db 745 GGTCCCAAGGTGTGCTGGTGTGACTGTGTAGAAAGATCATTTGTGACACCTATGGTGT 804
QY 860 TGGGGTGTCTATGGTGGTGGTCTTTCTCCGGGAAGGATCCACCAAGTTGATAGGAGT 919
Db 805 TGGGGCGCACATGGTGGTGGTCTCTCAGGCAAGGATTTCTCAAAGTTGATAGGCT 864
QY 920 GGTGCTTACATTTGTGAGACAGCTGCTAAGACATTTGGCAAGTGGAGTACCGAAGG 979
Db 865 GGTGCTTATGCGCGCTGGTGGTGGTGGCAAGTGGTGGTACCGCGGATTTGGCCAAAAGG 924
QY 980 TGCATTGTGCAAGTGTCTATGCAATTTGGTGTGCGCGAGCCTTTGTCTGTCTTTGTGAC 1039
Db 925 GCTTGGTGCAGTTCTCTATGCTATTGGGTTGCTGAACCCACCAAGCATTTATATAGAC 984
QY 1040 ACTATGGCACCGGGAAGATCCATGATAAGGAGATTTCTCAACATTTGTGAAGGAACTTT 1099
Db 985 ACTATGGGACATCTAAATTTGAGCACCGAAGCCCTTGTAGAAATTTATCAAGAAATAATTT 1044
QY 1100 GAATTCAGCCCGGTATGATCTCCATCAACCTTGATCT 1137
Db 1045 GACTTACGCCCTGGCGTAATTGTAAGAAATTAGATTT 1082

RESULT 15
US-09-489-039A-4746
; Sequence 4746, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIORITY FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4746
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4746

Query Match 20.7%; Score 306.8; DB 4; Length 1158;
Best Local Similarity 57.9%; Pred. No. 1.3e-84;
Matches 595; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 83 ACATTCCTATTATACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTCGACCAA 142
Db 10 AAACACCTTTTACGCTGTGATCCGCTATCAGAAAGGCATCTTGACAAATTCCTGACCA 69
QY 143 ATCTCCGATGCTGTCTCTCGACGCTTGCCCTTGAACAGGACCCAGACAGCAAGGTTGCTGC 202
Db 70 ATCTCCGATGCGGTGCTGATGCGATCCTCGAGCAGGATCCGAAAGCGGTGTGCGATGT 129
QY 203 GAAACATGACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAGGCCAAC 262
Db 130 GAAACCTATGTCAAAACCCGGCATGGTGGTGGTAGGCGCGAAATCACCAAGCGCATGG 189
QY 263 GTTGACTACGAGAAGATCGTGCTGACCTCGCAGGAACATCGGTTCTCGTCTCAACAGAT 322
Db 190 GTTGATATCGAAGAGATCACCGCAACACCGTCCGCGAAATTTGGCTACGTGCAATTCGGT 249
QY 323 GTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTGTAACATTTGAGCAGCAGCCCTGAT 382
Db 250 ATGGGGCTTTGAGCCCAACTCGTGGCGCGTACTGAGCGCCATTTGGCAAAACAGTCTCGGAC 309
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QY 383 ATTGCCCAGGGTGTGCACGGCCACCTTACCACAAAAGACCCGAGGAATCGGTCTGGAGAC 442
Db 310 ATTAACCAAGGCGGTGAGCCGTGCGCGAT-----CGGTGGAAACAGGCGCGCGGCAC 360
QY 443 CAGGGTCACATGTTTGGCTATGCCACGGAAGAAACCCAGAAATTCATGCCATTTGAGTCA 502
Db 361 CAGGGCTGATGTTTGGCTACGCCACTAAAGAAACCGACGTGCTGATGCGCGCGCGGTG 420
QY 503 GTTCTTGCAACTAAACTCGGTGCTCGTCTACCGAGGTTCCGAAAGACGGAACCTGCCCA 562
Db 421 ACTTACGCTCACCGTCTGGTGCAGGCTCAGAGTGAAGTCCGCTAAAGACGACACCTGCGG 480
QY 563 TGGTTGAGGCTGTGAGGAAACCCAAAGTGAAGTCTTGAAGTATTACAAATGACAAACGCTGCC 622
Db 481 TGGCTGGCGCCCGGATGCGAAAGCCAGGTGACCTTCCAGTATGACGACGCGCAAAATCGTC 540
QY 623 ATGGTTCCAGTTCGTGTCCACATGTGTCTATCTCCACCCCAACATGATGAGACTGTGACC 682
Db 541 G-----GCATCGACGCGTCTGTTCTGTGACTCAGACCGCGNAGATATCGAT 588
QY 683 AACGACGAAATTCGAGCTGACCTCAAGAGCATGTGATCAAGCCGGTATCCCGGAGAAG 742
Db 589 CAGAAATCCCTGCAGGAAGCAGTGTGAGAGAGATCATCAAGCCGATTTCTGCCGACCGAA 648
QY 743 TACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGGCGGTTTTGTCTATTGGAGGT 802
Db 649 TGGCTCAACGCGTCCACCAAAATTTCTCATCAACCCGACCGCGCGTTTCGTTATTGGCGGC 708
QY 803 CCTCAGGTGATGCTGTCTCAGCGCGCGCAAGATCATCATCGATCTTACGAGGATGG 862
Db 709 CCGATGGCGACTGCGGTCTGACCGGTGCTAAGATCATCGTTGATACCTACGCGGCATG 768
QY 863 GGTGCTCATGTGTGTGTGCTTTCTCCGGGAAGGATCCCAAGGTTGTAGAGTGT 922
Db 769 GCTGCCACGCGCGCGCGCTTCTCCGTTAAAGATCCATCTAAAGTTGACCGTTCGCGCA 828
QY 923 GCTTACATTTGAGACAGGCTGCTAAGAGCATTTGGCAAGTGGACTAGCCAGAAAGTGC 982
Db 829 GCCTACGCGCGCGCTATGTGGCAAGAACATCGTTGCCGAGGCTTGCCCGATCGTTGC 888
QY 983 ATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCTTTGTCTGCTTTTGTGACACC 1042
Db 889 GAAATTCAGGTTTCTACGCTATCGCGTTTCAGAAACCGACGTCCATCATGTGTGAAACC 948
QY 1043 TATGCAACCGGGAAGATCCATGATAAGAGATTTCTCAACATTTGTAAGGAACTTTGAT 1102
Db 949 TTTGGCACCGAGAAAGTGCCTTCTGAACAGCTGACCCCTGCTGGTGGTGGTCTTCGAC 1008
QY 1103 TTCAGGCC 1110
Db 1009 CTGCGTCC 1016
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Search completed: August 31, 2005, 06:13:11  
Job time : 254.414 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 21:30:39 ; Search time 995.128 Seconds  
(without alignments)  
9764.058 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
Sequence: 1 ACCCAAGCCCCCACTCAACCA.....CAAAAGAAATGTTCCAGTT 1485

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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19:	/cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20:	/cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21:	/cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
23:	/cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485	100.0	1485	20	US-10-734-698A-38
2	1485	100.0	1485	21	US-10-917-602A-38
3	1485	100.0	1518	17	US-10-431-252-1
4	1474.6	99.3	1496	18	US-10-425-114-11983
5	1464.6	98.6	1855	18	US-10-424-599-77204
6	1460.2	98.3	1465	18	US-10-425-114-10164
7	1208.6	81.4	1538	18	US-10-424-599-115395

8	1207.6	81.3	1509	18	US-10-425-114-29554	Sequence 29554, A
9	1205.2	81.2	1210	18	US-10-425-114-7305	Sequence 7305, Ap
10	1204.4	81.1	1488	18	US-10-425-114-7202	Sequence 7202, Ap
11	1204.4	81.1	1494	18	US-10-425-114-10112	Sequence 10112, A
12	1204.4	81.1	1505	18	US-10-425-114-11712	Sequence 11712, A
13	1204.4	81.1	1510	18	US-10-425-114-11050	Sequence 11050, A
14	1204.4	81.1	1514	18	US-10-425-114-8323	Sequence 8323, Ap
15	1204.4	81.1	1514	18	US-10-425-114-9591	Sequence 9591, Ap
16	1204.4	81.1	1514	18	US-10-425-114-10155	Sequence 10155, A
17	1204.4	81.1	1514	18	US-10-425-114-10248	Sequence 10248, A
18	1204.4	81.1	1515	18	US-10-425-114-8286	Sequence 8286, Ap
19	1204.4	81.1	1515	18	US-10-425-114-8296	Sequence 8296, Ap
20	1204.4	81.1	1515	18	US-10-425-114-9070	Sequence 9070, Ap
21	1204.4	81.1	1515	18	US-10-425-114-9087	Sequence 9087, Ap
22	1204.4	81.1	1515	18	US-10-425-114-9138	Sequence 9138, Ap
23	1204.4	81.1	1515	18	US-10-425-114-11285	Sequence 11285, A
24	1204.4	81.1	1515	18	US-10-425-114-12737	Sequence 12737, A
25	1204.4	81.1	1515	18	US-10-425-114-12745	Sequence 12745, A
26	1204.4	81.1	1523	18	US-10-425-114-10819	Sequence 10819, A
27	1204.4	81.1	1529	18	US-10-425-114-10266	Sequence 10266, A
28	1204.4	81.1	1529	18	US-10-425-114-12664	Sequence 12664, A
29	1202.8	81.0	1515	18	US-10-425-114-10041	Sequence 10041, A
30	1196.6	80.6	1495	18	US-10-425-114-10262	Sequence 10262, A
31	1195	80.5	1835	18	US-10-424-599-77205	Sequence 77205, A
32	1192.2	80.3	1489	18	US-10-425-114-7368	Sequence 7368, Ap
33	1191	80.2	1427	18	US-10-425-114-12787	Sequence 12787, A
34	1191	80.2	1456	18	US-10-425-114-8399	Sequence 8399, Ap
35	1191	80.2	1458	18	US-10-425-114-8336	Sequence 8336, Ap
36	1191	80.2	1461	18	US-10-425-114-8325	Sequence 8325, Ap
37	1191	80.2	1461	18	US-10-425-114-11194	Sequence 11194, A
38	1191	80.2	1468	18	US-10-425-114-10273	Sequence 10273, A
39	1189.4	80.1	1456	18	US-10-425-114-10701	Sequence 10701, A
40	1175.4	79.2	1459	18	US-10-425-114-9680	Sequence 9680, Ap
41	1145	77.1	1349	18	US-10-425-114-11199	Sequence 11199, A
42	1142.6	76.9	1349	18	US-10-425-114-11868	Sequence 11868, A
43	1132.8	76.3	1342	18	US-10-425-114-8517	Sequence 8517, Ap
44	1124.4	75.7	1436	18	US-10-424-599-77201	Sequence 77201, A
45	938.2	63.2	1084	18	US-10-425-114-8006	Sequence 8006, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-734-698A-38  
; Sequence 38, Application US/10734698A

; Publication No. US20040209341A1

; GENERAL INFORMATION:

; APPLICANT: FALCO, SAVERIO CARL

; ALLEN, STEPHEN M.

; RAFALSKI, J. ANTONI

; HITZ, WILLIAM D.

; KINNEY, ANTHONY J.

; ABELL, LYNE N.

; THORPE, CATHERINE J.

; TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD VERSION 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/734,698A

; FILING DATE: 12-Dec-2003

; CLASSIFICATION: <Unknown>

















Qy	1406	ATGATCAACTAAAAA-ATGTACTCTCTGTTT-----TCGACCATTGTGTCTCTTA	1455
Db	1419	GTGATCAACTAAAAACATGTACTCTCTGTTTGTATGTATGCGCCTTACCAATGTGTCTCTTA	1478
Qy	1456	ATATCAGTATCAAAAAGAATGT	1477
Db	1479	ATATCAATATCAAAAAGAGAGT	1500

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RESULT 9
US-10-425-114-7305
; Sequence 7305, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7305
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700649594_FLI
US-10-425-114-7305

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Query Match	81.2%;	Score 1205.2;	DB 18;	Length 1210;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1207;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	276	AGATCGTGGTGCACACCTGCAGGACATCGGCTTCGTCTCAAAAGATGTGGGACATTGATG	335	
DB	1	AGATCGTGGTGCACACCTGCAGGAAACATTCGGCTTCGTCTCAAAAGATGTGGGACATTGATG	60	
QY	336	CTGACAACTGCAAGGTCCCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCACAGGGTG	395	
DB	61	CTGACAACTGCAAGGTCCCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCACAGGGTG	120	
QY	396	TGCA CGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGAGACACAGGGTCACATGT	455	
DB	121	TGCA CGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGAGACACAGGGTCACATGT	180	
QY	456	TTGGCTATGCCACGAGCAAGAAACCCAGAAATTGATGCCATTGAGTCATGTTCTTGCAACTA	515	
DB	181	TTGGCTATGCCACGAGCAGAGCCCGAGAAATTGATGCCATTGAGTCATGTTCTTGCAACTA	240	
QY	516	AACTCGGTGCTCGTCTCACCGAGGTTGCCAAGAACGGAACTGTGCCCATGGTTGAGGCCGTG	575	
DB	241	AACTCGGTGCTCGTCTCACCGAGGTTGCCAAGAACGGAACTGTGCCCATGGTTGAGGCCGTG	300	
QY	576	ATGGGAACCCCAAGTGACTGTGAGTATTACATGACACGGTGCCATGGTTCCAGTTC	635	
DB	301	ATGGGAAGACCCCAAGTGACTGTGAGTATTACATGACACGGTGCCATGGTTCCAGTTC	360	
QY	636	GTGTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTG	695	
DB	361	GTGTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTG	420	
QY	696	CAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAGAAAGTACTCTTGATGAGA	755	
DB	421	CAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAGAAAGTACTCTTGATGAGA	480	
QY	756	AGACCAATTTTCCACTTGAACCCCTCTGGCCGGTTTTGTGCTATTGGAGGTCCTCACGGTGATG	815	

Db	481	AGACCATTTTCCACTTGAAACCCCTCTGGCCGTTTTGTCTCATGTGAGGTCCTCAGCGTGATG	540
Qy	816	CTGGTCTCACGGCCGCAAGATCATCATGATACTATTACGGAGGATGGGTGCTCATGGTG	875
Db	541	CTGGTCTCACGGCCGCAAGATCATCATGATACTATTACGGAGGATGGGTGCTCATGGTG	600
Qy	876	GTGGTGCTTCTTCGGGAAGGATCCCAAGAGTTGATAGGAGTGGTGCTTACATTGTGTGA	935
Db	601	GTGGTGCTTCTTCGGGAAGGATCCCAAGAGTTGATAGGAGTGGTGCTTACATTGTGTGA	660
Qy	936	GACAGGCTGCTAAGAGCATTTGCGCAAGTGGCATAGCCAGAAGTGCTATGTGCACAGTGT	995
Db	661	GACAGGCTGCTAAGAGCATTTGCGCAAGTGGCATAGCCAGAAGTGGCATTTGTGCACAGTGT	720
Qy	996	CTTATGCCATTGGTGTGCCGAGACCTTTGTCTCTTTTGTGTGACACCTATGGCACCGGGA	1055
Db	721	CTTATGCCATTGGTGTGCCGAGCCTTTGTCTCTTTTGTGTGACACCTATGGCACCGGGA	780
Qy	1056	AGATCCCATGATAGGAGGATTTCTCAACATTTGTGAAGGAGAACTTTTGATTTTCAGGCCCGGTA	1115
Db	781	AGATCCCATGATAGGAGGATTTCTCAACATTTGTGAAGGAGAACTTTTGATTTTCAGGCCCGGTA	840
Qy	1116	TGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACACAGTTCTTTGAAACACTGCTG	1175
Db	841	TGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACACAGTTCTTTGAAACACTGCTG	900
Qy	1176	CATATGACACTTTCCGCAGAGAGACCCCTGACATTCACTGGGAAGTGGTCAAGCCCTCA	1235
Db	901	CATATGACACTTTCCGCAGAGAGACCCCTGACATTCACTGGGAAGTGGTCAAGCCCTCA	960
Qy	1236	AGTGGGAGAAGGCTTAAGGCCATTTCATTCCACTGCAATGTGCTGGAGTTTTTATGCGTT	1295
Db	961	AGTGGGAGAAGGCTTAAGGCCATTTCATTCCACTGCAATGTGCTGGAGTTTTTATGCGTT	1020
Qy	1296	GCCCTTATAATGCTATTATCCATAACTTTCCAGTCCCTTGCTGTGTGTTTTTCTCTCG	1355
Db	1021	GCCCTTATAATGCTATTATCCATAACTTTCCAGTCCCTTGCTGTGTGTTTTTCTCTCG	1080
Qy	1356	TCGTCTCTCTCTATTTTGTCTCTGCTTTCATTTGTAATTTTTTATCATCATCAACT	1415
Db	1081	TCGTCTCTCTCTATTTTGTCTCTGCTTTCATTTGTAATTTTTTATCATCATCAACT	1140
Qy	1416	AAAAATGTACTCTCTGTTTTCCGACCATTTGTCTCTTAATATCAGTATCAAAAAAGAT	1475
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Qy	1476	GTTCCEAGTT	1485
Db	1201	GTTCCEAGTT	1210

RESULT 10  
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US-10-425-114-7202  
; Sequence 7202, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 7202  
; LENGTH: 1488  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:



; OTHER INFORMATION: Clone ID: 700649684\_FLI  
US-10-425-114-7202

Query Match 81.1%; Score 1204.4; DB 18; Length 1488;  
Best Local Similarity 91.9%; Pred. No. 0;  
Matches 1343; Conservative 0; Mismatches 101; Indels 18;

Qy	29	CTCTCTGTGCTTCCTTCTCACTTTTAAAGTATTAGATGGCGAGACATTC	88
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Qy	89	CTATTTACCTCAGAGTCAGTGAAACGAGGGAACCCCTGCACAAGCTCTCGACCAAATCTCC	148
Db	83	CTATTTACCTCAGAGTCGGTGAAACGAGGGAACCCCTGCAAGCTCTGGACCAAATCTCC	142
Qy	149	GATGCTGTCTCGACGCTTGCTTTGAAACAGGACCAGACAGCAAGGTTGCTTCGGAACA	208
Db	143	GATGCTGTCTCGACGCTTGCTTCGAGCAGGACCAGACAGCAAGGTTGCTTCGGAACA	202
Qy	209	TGCACCAAGACCAACTTGGTTCATGCTCTTCGGAGAGATCACCAACCAAGGCCAAGTTGAC	268
Db	203	TGCACCAACCAACTTGGTTCATGCTCTTCGAGAGATCACGACCAAGGCCAAGTTGAC	262
Qy	269	TACAGAAGATCGTGCGTGACACTCGAGGAAATACGCGTTTCGTCAAAAGATGTGGGA	328
Db	263	TACAGAAGATAGTGTGCTGACACTCGAGGAAATCATCGCTTCGTCAAAATGATGTGGGA	322
Qy	329	CTTGATGCTGACRACTCGAAGTCTTGTAAACATTTGAGCAGCAGAGCCCTGATATTGCC	388
Db	323	CTTGATGCGCAACTCGAAGTCTCGTCAACATTTGAGCAGCAGAGCCCTGATATTGCT	382
Qy	389	CAGGGTGTGACGGCGCACCTTTACCAAAGACCCGAGGAAAATCGGTGTGTGGAGACAGGGT	448
Db	383	CAGGGTGTACACGGCCACCTTACCAAANAACCTGAAGAAATTGTGTGGTAGCAGGGT	442
Qy	449	CACATGTTTGGCTATGCCACGGACGAAACCCCAGAAATGTATGCOATTTGATGTCCTT	508
Db	443	CACATGTTTGGCTATGCGCACTGATGAACCCCTGAAATTTGATGCCATTTGAGCATTTCTT	502
Qy	509	GCAACTAAACTCTGGTGTCTGCTCACCGAGGTTTCGCAAGAACGAACTGCCCCATGTTG	568
Db	503	GCAACAAACTCTGGTGTCTGCTCACCGAGGTTTCGCAAGAACGTACTGCCCCTTGCTG	562
Qy	569	AGGCCTGATGGGAAAAACCAAGTGACTGTTGAGTATTACAATGACAAACGTTGCCATGGT	628
Db	563	AGGCCTGATGGGAAAGACCAAGTGACCGTTGAGTATTACAATGACAAATGTTGCCAGGTT	622
Qy	629	CCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTGACCAACGAC	688
Db	623	CCTATTCTGTAPACACACCGTGCTAATCTCCACCCCAACACGACGAGACTGTCAACCAATGAC	682
Qy	689	GAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAGAACTACCTT	748
Db	683	GAAATTGCTGTGACCTCAAGAGCATGTGATCAAGCCTGTGATCCCGAGAACTACCTT	742
Qy	749	GATGAGAAGACCATTTTCCAATTGAAACCCCTCTGGCCGTTTTGTTCATTGGAGGTCCTCAC	808
Db	743	GATGAGAAGACCAATTTTCCAATTGAAACCCCTTCAGGCCGTTTTGTTCATTGGTGGCCCTCAT	802
Qy	809	GGTCATGCTGTGCTCACCGGCCGAAGATCATCATCGATCTTACGAGGAGATGGGGTGCT	868
Db	803	GGCGATGCTGTGCTCACCGGCCGCAGATCATTTATCGATCTTATGAGGAGATGGGGTGCT	862
Qy	869	CATGGTGGTGGTCTTCTCCGGAAAGGATCCCAACCAAGGTTGATAGGAGTGGTGCTTAC	928
Db	863	CATGGTGGTGGTCTTCTCCGGAAAGGACCCCTCAAGGTTGATAGGAGTGGTGCTTAC	922
Qy	929	ATTCTGACACAGGCTGCTTAAGACATTTGGCAAGTGGACTAGCCAGAGGTGCATTGTG	988
Db	923	ATTGTGACACAGGCTGCTTAAGACATTTGGCAAGTGGACTTGGCAGAGGTGCATTGTG	982
Qy	989	CAAGTGTCTTATGCCATTTGGTGTGCCCGAGCCCTTTGTCTGTCTTTGTTTGAACCTATGGC	1048

983	CAAGTGTCTTATGCCATTGGTGTGCCTGAGCCTTTGTCGTGTTGTTGTACACCTATGGC	104
1049	ACCGGGAAGATCCATGATAAGAGAGATCTCAACATTTGTGAAGAGAACTTTTGATTTTCAGG	1108
1043	ACTGGGAAGATCCATGATAAGAGAGATTCTCAACATTTGTGAAGGAAACCTTTGATTTTCAGG	1102
1109	CCGGGTATGATCTCCATCAACCTTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTTGAAG	1168
1103	CCTGGTATGATCTCCATCAACCTTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTTGAAG	1162
1169	ACTGCTGCATATGGACACATTTCCGACAGAGAGACCCCTGACTTCAATGCGGAAGTGGTCAAG	1228
1163	ACTGCTGCCTTATGGACACATTTTGAAGAGAGAAGCCCTGACTTCAATGCGGAAGTGGTCAAA	1222
1229	CCCTCAAGTGGGAGAAAGGCTTAAGGCCATTCAATCCACTGCAATGCTCTGGAGAGTTTTT	1288
1223	CCCTCAAGTGGGAGAAAGGCTTAA-GTAATTCATTTCCACTGCTCATGCTGGGAAGTTTTT	1381
1289	T-AGCGTTGGCCCTTATA--ATGTCTATATTCATAACTTTCCACGTCCTCTGCTCTGTGT	1345
1282	TGAGCGTTGGCCCTTATAATATGCTAATATCCATACTTTCCACGCTCTTACTCTGTGT	1341
1346	TTTTCTCTCGTGTGCTCTCCTTAATTTTGTGTTCTCTCGCCTTTCAATTTGPAATTTTTTAC	1405
1342	GTTTCTCTCCTCTCTCTCTTAATTTTGTGTTATTTGT-ATGTTCTTTTGTGPAATTTTTTAC	1397
1406	ATGATCAACTAAAAA-ATGFPACTCTCTGTTT-----TCCGACCATTGTCGTCTCTTA	1455
1398	GTGATCAACTAAAAAATGFPACTCTCTCTGTTTGTATGATGCCCTACCAATGTCGTCTCTTA	1457
1456	ATATCAGTATCAAAAAGAAATGT	1477
1458	ATATCAATATCAAAAAGAGAGT	1479

## RESULT 11

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US-10-425-114-10112
; Sequence 10112, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10112
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700894196_FLI
US-10-425-114-10112

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	Query Match	81.1%	Score 1204.4	DB 18	Length 1494
	Best Local Similarity	91.9%	Pred. No. 0		
	Matches 1343	Conservative	0	Mismatches 101	Indels 18
				Gaps 6	
QY	29	CTCTCTGCTCTCTCTCTACCTTCCAAAGTTTTTAAAGTATTAAAGTGGCAGAGACATTC	88		
DB	29	CCCTTTCTGCTCTCTCTCTACCTTCCAAAGTTTTTAAAGTATTAAAGTGGCAGAGACATTC	88		
QY	89	CTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGTCTCGCACCAATCTCC	148		
DB	89	CTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGTCTCGCACCAATCTCC	148		
QY	149	GATGCTGTCTCGACGCTTGCTTGAAACAGGACCCAGACAGCAAGGTTCCTCGCAACA	208		



Db 149 GATGCTGCTCGACGCTTGCCTCGAGCAGGACCCGACAGCAAGTGTGCTCGGAACA 208  
QY 209 TGCAACAAAGCAACTTGGTCTATGGTCTTCGGAGAGATCACCAAGGCAAGGTTGAC 268  
Db 209 TGCAACAAAGCAACTTGGTCTATGGTCTTCGGAGAAATCACAGCAAGGCAAGGTTGAC 268  
QY 269 TAGCAGAGATCGTGGTGTACACCTGCAGGAACATCGGCTTCCTCAACGATGTGGGA 328  
Db 269 TAGCAGAGATAGTGGTGTACACCTGCAGGAACATCGGCTTCCTCAACGATGTGGGA 328  
QY 329 CTTGATGCTGACAACTGCAAGTCTTGTAAACATTTGAGCAGAGAGCCCTGATATTGCC 388  
Db 329 CTTGATGCTGACAACTGCAAGTCTTGTAAACATTTGAGCAGAGAGCCCTGATATTGCC 388  
QY 389 CAGGGTGTGACCGGCACCTTACCAAAAGACCCGAGGAATCGGTCTGGAGACCAAGGT 448  
Db 389 CAGGGTGTACCGGCACCTTACCAAAAGACCCGAGGAATCGGTCTGGAGACCAAGGT 448  
QY 449 CACATGTTGGCTATGCCAGCGAACCACCGAATTTGATGCCATTTGATCTATGTTCTT 508  
Db 449 CACATGTTGGCTATGCCAGCGAACCACCGAATTTGATGCCATTTGATGCTATGTTCTT 508  
QY 509 GCAACTAACTCGGTGCTCTCACCGAGTTTGCAGAAACCGAACCTGCCCATGGTTG 568  
Db 509 GCAACAAACTCGGTGCTCTCACCGAGGTTTGCAGAAACCGGTACCTGCCCTTGGCTG 568  
QY 569 AGSCCTGATGGGAAACCCCAAGTGTGTTGAGTATTACAAATGACACGCGTGCATGGTT 628  
Db 569 AGSCCTGATGGGAAACCCCAAGTGTGTTGAGTATTACAAATGACATGATGGTGCAGGGTT 628  
QY 629 CCAAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGAC 688  
Db 629 CCTATTTCGTGTACACACCGTGTCTAATCTCCACCAACACGACGAGACTGTGACCAATGAC 688  
QY 689 GAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGTGTATCCCGGAGAGTACCTT 748  
Db 689 GAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGTGTATCCCGGAGAGTACCTT 748  
QY 749 GATGAGAAGACCAATTTTCACTTGAACCCCTCTGGCCGTTTGTCTCAATGAGGCTCTCAC 808  
Db 749 GATGAGAAGACCAATTTTCACTTGAACCCCTCTAGCCGTTTGTCAATGAGGCTCTCAT 808  
QY 809 GGTGATGCTGGTCTCACCGCCGCAAGATCATCATGACTTACCGAGGATGGGTGCT 868  
Db 809 GGGATGCTGGTCTCACCGCCGCAAGATCATTTATCGATATTATGAGGATGGGTGCT 868  
QY 869 CATGGTGGTGGTCTTCTCCGGGAAGATCCCAAGGTTGATAGGAGTGCTGCTTAC 928  
Db 869 CATGGTGGTGGTCTTCTCCGGGAAGGACCTTACCAAGGTTGATAGGAGTGCTGCTTAC 928  
QY 929 ATTGTGAGACAGGCTGCTAAGACATTTGGCAAGTGGACTAGCCAGAGAGGTCATTGG 988  
Db 929 ATTGTGAGACAGGCTGCTAAGACATTTGGCAAGTGGACTTGCAGAGAGGTCATTGG 988  
QY 989 CAAAGTCTTATGCCATTTGGTGTGCGGAGCCTTGTCTGTCTTTGTGACACCTATGGC 1048  
Db 989 CAAAGTCTTATGCCATTTGGTGTGCGCTGAGCCTTGTCTGTGTTGTGACACCTATGGC 1048  
QY 1049 ACCGGAAGATCATGATAGGAGATTCTCAACATTTGTGAAGAGAACTTTGATTTGAGG 1108  
Db 1049 ACTGGGAAGATCATGATAGGAGATTCTCAACATTTGTGAAGAGAACTTTGATTTGAGG 1108  
QY 1109 CCGGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATACAGGTTCTTGAAG 1168  
Db 1109 CCGGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATACAGGTTTGAAG 1168  
QY 1169 ACTGCTGCATATGGACACTTTCGCGAGAGAGACCTTGCATCTTCAATGGGAAGTGGTCAAG 1228  
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QY 1229 CCCTCAAGTGGGAGAGGCTTAAGGCCATTTCAATCCATGTCATGCTGGAGGTTTTT 1288

Db 1229 CCCTCAAGTGGGAGAGGCTTAA-GTAATTCATTCACCTGCTGTATGCTGGAAGTTTTT 1287  
QY 1289 T-AGCGTTGCCCTTATA--ATGCTATTATCCATACTTTCCACGTCCTTGTCTGTGT 1345  
Db 1288 TGAGCGTTGCCCTTATAATATGCTTAATATCCATACTTTCCACGTCCTTACTCTGTGT 1347  
QY 1346 TTTTCTCTCGTCT 1405  
Db 1348 GTTCT 1403  
QY 1406 ATGATCACTAAATAA-ATGCTACTCTCTGTTT-----TCCGACCATGCTCTCTTA 1455  
Db 1404 GTGATCACTAAATAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTA 1463  
QY 1456 ATATCAGTATCAAAAAGATGT 1477  
Db 1464 ATATCATATCAAAAAGAGAT 1485

RESULT 12  
US-10-425-114-11712  
; Sequence 11712, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 11712  
; LENGTH: 1505  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701123183\_FLI  
US-10-425-114-11712

Query Match 81.1%; Score 1204.4; DB 18; Length 1505;  
Best Local Similarity 91.9%; Pred No. 0;  
Matches 1343; Conservative 0; Mismatches 101; Indels 18; Gaps 6;

QY 29 CT 88  
Db 40 CCCTTTCT 99  
QY 89 CTATTTACCTCAGATCTAGTGAACGAGGACACCTCTGACAGCTCTGCGACCAATCTCTC 148  
Db 100 CTATTTACCTCAGATCTAGTGAACGAGGACACCTCTGACAGCTCTGCGACCAATCTCTC 159  
QY 149 GATGCTGTCTCGACGCTTTCCTTCAACAGGACCCAGCAGCAAGTGTCTCTCGGAAACA 208  
Db 160 GATGCTGTCTCGACGCTTTCCTTCAACAGGACCCAGCAGCAAGTGTCTCTCGGAAACA 219  
QY 209 TGCACCAAGACCAACTTGGTCTATGGTCTTTCGAGAGATCACCAAGGACCAAGTGTGAC 268  
Db 220 TGCACCAAAACCAACTTGGTCTATGGTCTTTCGAGAAATCACGACCAAGGACCAAGTGTGAC 279  
QY 269 TAGCAGAGATCGTGGTGTACACCTTGCAGGAACATCGGCTTCTCTCAACCATGTTGGA 328  
Db 280 TAGCAGAGATAGTGGTGTACACCTTGCAGGAACATCGGCTTCTCTCAATGATTTGGA 339  
QY 329 CTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGAGCCCTGATATTGCC 388  
Db 340 CTTGATGCTGACAACTGCAAGGTCCTTGTCAACATTTGAGCAGCAGAGCCCTGATATTGCC 399  
QY 389 CAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAATCGGTGCTGGAGACCAAGGT 448



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Db 645 CCTATTGCTGACACACCGTGCTAAATCTCACCACACACAGAGACTGTCCACATGAC 704
Qy 689 GAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAGAGTACCTT 748
Db 705 GAAATTCGCTGACCTCAAGAGCATGTGATCAAGCCGTGTATCCAGAGAGTACCTT 764
Qy 749 GATGAGAGACCAATTTTCACCTTGAACCCCTCTGGGCGTTTGTCTCATTTGGAGTCTCTAC 808
Db 765 GATGAGAGACCAATTTTCACCTTGAACCCCTCTAGGCGGTTTGTCTCATTTGGTGGCCCTCAT 824
Qy 809 GGTGATGCTGCTCTACCGGCGCAGAGATCATCATGATCTTACCGAGAGTGGGTGCT 868
Db 825 GGGCATGCTGCTCTACCGGCGCAGAGATCATCATGATCTTATGAGAGTGGGTGCT 884
Qy 869 CATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGGTTGATAGGAGTGGTCTTAC 928
Db 885 CATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGGTTGATAGGAGTGGTCTTAC 944
Qy 929 ATTGTGAGACAGCTGCTAAGAGCATTTGGGCAAGTGGACTAGCCAGAGAGTGCATTTGG 988
Db 945 ATTGTGAGACAGCTGCTAAGAGCATTTGGGCAAGTGGACTTGCACACCTATGCG 1048
Qy 989 CAAAGTCTTATGCCCATTTGGTGGCGGAGCCTTCTGCTGCTTGTGTCGACACCTATGCG 1048
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Qy 1049 ACCGGAAGATCATGATGAAGAGATTTCTCAACATTTGGAAGGAGAACTTTGATTTGAG 1108
Db 1065 ACTGGGAAGATCATGATGAAGAGATTTCTCAACATTTGGAAGGAGAACTTTGATTTGAG 1124
Qy 1109 CCGGTTATGATCTCCATCAACCTTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTTGAAG 1168
Db 1125 CCGGTTATGATCTCCATCAACCTTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTTGAAG 1184
Qy 1169 ACTGTCGATATGACACATTTGGCAGAGAGGACCTGACTTACATGGAGTGGTCAAG 1228
Db 1185 ACTGTCGATATGACACATTTGGCAGAGAGGACCTGACTTACATGGAGTGGTCAAA 1244
Qy 1229 CCGCTCAAGTGGGAGAGGCTTAAGGCCATTTCAATCCATGCAATGCTGGAGTTTTT 1288
Db 1245 CCGCTCAAGTGGGAGAGGCTTAAGGCCATTTCAATCCATGCAATGCTGGAGTTTTT 1303
Qy 1289 T-AGGCTTCCCTTATA--ATGCTATATTCATATACTTTCACGCTTCTGCTGCT 1345
Db 1304 TGAGCGTTCGCTTATAATATGCTAAATATCCATAACTTTCACGCTTCTTACTCTGCT 1363
Qy 1346 TTTTCTCTGCTGCTCCTCTATTTTGTCTCTGCTTTCATTTGTAATTTTAC 1405
Db 1364 GTTCTCTCTCTCTCTCTCTATTTTGTATTTGT-----ATGTTCTTTTGTAAATTTTAC 1419
Qy 1406 ATGATCAACTAAAAA-ATGATCTCTCTGTT-----TCGGACCATTTGTCTCTTA 1455
Db 1420 GTGATCAACTAAAAAATGATCTCTCTGTTGTATGATGCTCCCTACCAATGCTCTCTTA 1479
Qy 1456 ATATCAAGTATCAAAAAGATG 1477
Db 1480 ATATCAATATCAAAAAGAGAGT 1501
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## RESULT 14

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US-10-425-114-8323
; Sequence 8323, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8323
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700747484_FLI
US-10-425-114-8323
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Query Match 81.1%; Score 1204.4; DB 18; Length 1514;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 101; Indels 18; Gaps 6;
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Qy 29 CTCTCTGCTCTCTCTTCTTACCTTTTCAAGTTTTTAAAGATTAAAGATGCGAGAGACATTC 88
Db 49 CCTTTCTGCTCTCTCTTCTTACCTTTTCAAGTTTTTAAAGATTAAAGATGCGAGAGACATTC 108
Qy 89 CTATTATACCTCAGAGTCAAGTGAACGAGGAGACACCTCTGACCAAGCTCTGCGACCAAAATCTCC 148
Db 109 CTATTATACCTCAGAGTCAAGTGAACGAGGAGACACCTCTGACCAAGCTCTGCGACCAAAATCTCC 168
Qy 149 GATGCTGCTCTGACGCTTTCCTTGAACAGGACCCAGACAGCAAGTTCCTGCGGAAAACA 208
Db 169 GATGCTGCTCTGACGCTTTCCTTGAACAGGACCCAGACAGCAAGTTCCTGCGGAAAACA 228
Qy 209 TGCACCAAGACCAACTTGGTCTATGCTCTTCCGAGAGATCACCACCAAGCCCAACGTTGAC 268
Db 229 TGCACCAAGACCAACTTGGTCTATGCTCTTCCGAGAGAAATCACCACCAAGCCCAACGTTGAC 288
Qy 269 TACGAGAAAGATCGTGGTGAACACCTCTGAGGAAACATCGGCTTCTCTCAACGATGTGGGA 328
Db 289 TACGAGAAAGATAGTGGTGAACACCTCTGAGGAAACATCGGCTTCTCTCAACGATGTGGGA 348
Qy 329 CTTGATGTGCAACATGCAAGTCTCTTGAACATTTAGTACGAGAGCCCTGATATGCTT 388
Db 349 CTGGATGCGGACCAACTGCAAGGCTCTCTGCAACATTTAGAGCAGAGAGCCCTGATATGCT 408
Qy 389 CAGGCTGTCAGCGGACCTTACCAAAAGACCCGAGGAAATCGGTCTGGAGACCAAGGT 448
Db 409 CAGGCTGTCAGCGGACCTTACCAAAAGACCCGAGGAAATCGGTCTGGAGACCAAGGT 468
Qy 449 CACATGTTGGTATGCCACGAGCAACCCAGAAATTTGATGCCATTTGATGATGCTTCTT 508
Db 469 CACATGTTGGTATGCCACGAGCAACCCAGAAATTTGATGCCATTTGATGATGCTTCTT 528
Qy 509 GCAACTAAATCGGTGCTCTCAACGAGGTTCCGAAAGAACGGAACCTGCGCATGTTG 568
Db 529 GCAACTAAATCGGTGCTCTCAACGAGGTTCCGAAAGAACGGAACCTGCGCATGTTG 588
Qy 569 AGGCTGATGGGAAACCCAGAGTACTTGTAGTATTAACAATGACAACGTCGCTGCTT 628
Db 589 AGGCTGATGGGAAACCCAGAGTACTTGTAGTATTAACAATGACAACGTCGCTGCTT 648
Qy 629 CCAGTTCTGTCCACATGCTTATCTCCACCCCAACATGATGAGATGTCGACCAACGAC 688
Db 649 CCTATTCTGTATACACACCGTGTCTATCTCCACCCCAACGAGAGTGTCTACCAATGAC 708
Qy 689 GAAATTCGAGTACCTCAAGGAGCATGATGATCAAGCCGGTATCCCGGAGAGTACCTT 748
Db 709 GAAATTCGAGTACCTCAAGGAGCATGATGATCAAGCCGGTATCCCGGAGAGTACCTT 768
Qy 749 GATGAGAGACCAATTTTCCACTTGAACCCCTCTGCGCTTTTGTCTATTTGGAGTCTTAC 808
Db 769 GATGAGAGACCAATTTTCCACTTGAACCCCTCTGCGCTTTTGTCTATTTGGTGGCTCAT 828
Qy 809 GGTGATGCTGCTCTCACCGGCGGCAAGATCATCATGATCTTACGAGGAGTGGGTGCT 868
Db 829 GGCATGCTGCTCTCACCGGCGGCAAGATCATCATGATCTTACGAGGAGTGGGTGCT 888
Qy 869 CATGCTGCTGCTCTTCTCCGGGAAGGATCCCAAGGTTGATGAGAGTGGTCTTAC 928
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**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
1	2083	75	8		2	AAW97743	Soybean S
2	1947	70.9			3	AAG40366	Arabidops
3	1946	70.8			2	AAW97742	Corn S-ad
4	1940	70.6			3	AAG06584	Arabidops
5	1935	70.4			3	AAG07760	Arabidops
6	1935	70.4			3	AAG37871	Arabidops
7	1900.5	69.2			3	AAG43921	Zea mays
8	1900.5	69.2			2	AAW34542	S-adenosy
9	1900.5	69.2			2	AAW34540	S-adenosy
10	1891.5	68.8			2	AAW97744	Wheat S-a

PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine  
 PT synthase; threonine deaminase; S-adenosylmethionine synthetase.  
 XX Example 7; Page 67-68; 98pp; English.

XX This is the amino acid sequence of a full-length soybean S-  
 CC adenosylmethionine synthetase, as deduced from a cDNA clone (see  
 CC AAX07184), designated s2.12b06, obtained from a soybean seed cDNA  
 CC library. The soybean enzyme shows sequence similarity to the tomato  
 CC enzyme. The invention relates to new isolated nucleic acid fragments (see  
 CC AAX07166-85) encoding plant enzymes (see AAW97727-44) that catalyze steps  
 CC in the biosynthesis of lysine, threonine, methionine, cysteine and  
 CC isoleucine from aspartate, the enzyme being selected from  
 CC dihydropicolinate reductase, diaminopimelate epimerase, threonine  
 CC synthase, threonine deaminase or S-adenosylmethionine synthetase. The  
 CC invention also relates to the construction of a chimeric gene encoding  
 CC all or a portion of the biosynthetic pathway enzyme, in sense or  
 CC antisense orientation, where expression of the chimeric gene results in  
 CC production of altered levels of the enzyme in a transformed host cell.  
 CC Overexpression or reduction of expression of genes encoding the amino  
 CC acid biosynthetic pathway enzymes in crop plants such as corn, soybean  
 CC and wheat can be used to alter levels of the amino acids in human food  
 CC and animal feed. Transformed host cells can also be used to identify  
 CC compounds that inhibit one of the enzymes

XX Sequence 392 AA;

#### Alignment Scores:

Pred. No.: 6.19e-201 Length: 392  
 Score: 2083.00 Matches: 392  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 75.80% Indels: 0  
 DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x AAW97743 (1-392)

QY 74 ATGGCAGACATCTCTATTACCTCAGATCAGTGAACGAGGACACCTCAGAGCTC 133  
 DB 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20  
 QY 134 TGGCACCAATCTCCGATCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAG 193  
 DB 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40  
 QY 194 GTTGCTCGCAACATGCAACAGCAACCTTGCTCATGGTCTTCGAGAGATCAACCAC 253  
 DB 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60  
 QY 254 AAGGCCAAGTTGACTACGAGAGATCGCTGCGTACACCTCGAGGACATCGGCTCGTC 313  
 DB 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80  
 QY 314 TCAACGATGTGGACTTGTGCTGACAACTGCAAGTCTTGTAAACATTGACAGAGAG 373  
 DB 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100  
 QY 374 AGCCCTGATATTGCCCGGCTGTCACGGCCACCTTTACCAAGACCCGAGGAATTCGGT 433  
 DB 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120  
 QY 434 GCTGGAGACCGGTTACATGTTGGCTATGCCAGGAGAAACCCAGAAATTGATGCCA 493  
 DB 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140  
 QY 494 TTGAGTCATGTTCTTCAACTAACTCCGCTGCTCCTCAGCGAGGTTCGCAAGAACGGA 553  
 DB 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160  
 QY 554 ACTGCCCCATGTTGAGGCTGATGGGAAACCCAAAGTGAATTCATGATGAC 613  
 DB 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180

QY 614 AACGGTCCATGGTTCCAGTTGCTGCACACTGTGCTTATCTCCACCCCAACATGATGAG 673  
 DB 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200  
 QY 674 ACTGTGACCAACGACGAAATTCGACCTCAAGGAGCATGTGATCAAGCCCGGTGATC 733  
 DB 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220  
 QY 734 CCGAGAAAGTACCTTGATGAGAAGACCATTTTCCACTTGAAACCCCTCTGGCGGTTTGT 793  
 DB 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240  
 QY 794 ATTGAGGTCTCTCAGGGTGATGCTGCTCACCAGCCGCAAGATCATCATCGATACTTAC 853  
 DB 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260  
 QY 854 GGAGATGGGTGCTCATGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGAT 913  
 DB 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280  
 QY 914 AGGAGTGTGCTTACATTGTGAGACAGCTCTTAAGACATTGGCAAGTGGACTAGCC 973  
 DB 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300  
 QY 974 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCCTTGTGCTCTTT 1033  
 DB 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320  
 QY 1034 GTTGACACCTATGGCACCGGGAAGATCCATGATGAAGAGATTCTCAACATTGTGAAGAG 1093  
 DB 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340  
 QY 1094 AACTTTGATTTTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAAT 1153  
 DB 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360  
 QY 1154 AACAGGTTCTTGAAGACTGCTGCATATGACACATTCGGCAGAGAGGCCCTGACTTCACA 1213  
 DB 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380  
 QY 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 DB 381 TrpGluValValLysProLeuLysTrpGluLysAla 392

RESULT 2  
 AAG40366  
 ID AAG40366 standard; protein; 393 AA.  
 XX AC AAG40366;  
 XX DT 18-OCT-2000 (first entry)  
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 50077.  
 XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX OS Arabidopsis thaliana.  
 XX PN EP1033405-A2.  
 XX PD 06-SEP-2000.  
 XX PF 25-FEB-2000; 2000EP-00301439.  
 XX PR 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126264P.  
 PR 29-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.



PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135829P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139452P.  
PR 17-JUN-1999; 99US-0139453P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
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DB 62 ThrIleAspTyrGluLysIleValArgAspThrCysArgSerIleGlyPheIleSerAsp 81
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QY 380 GATATTGCCAGGTTGTCACGCCACACCTTACCAGAGACCCGAGGAATCGGTGCTGGA 439
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QY 500 CATGTTCTTGCACAACTAACTCGGTGCTCGTCTCACCGAGGTTCCGAGAACCGAACCTGC 559
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KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff.
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PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 30-AUG-1999; 99US-0151080P.  
PR 31-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.

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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1,77e-182 Length: 392
Score: 1900.50 Matches: 356
Percent Similarity: 96.12% Conservative: 16
Best Local Similarity: 91.99% Mismatches: 14
Query Match: 69.16% Indels: 1
DB: 3 Gaps: 1

US-10-734-698A-38 (1-1485) x AAG43921 (1-392)

QY 77 GCAGAGACATCTCTATTACCTCAGTCAAGACGAGGACACCTCAGACGCTCTGC 136
DB 3 AlaGluSerPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22

QY 137 GACCAATCTCCGATCTGCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTT 196
DB 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal 42

QY 197 GCCTGCGAAACATGACACCAAGACCAACTTGGTCATGCTCTCGAGAGATCACCAAG 256
DB 43 AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrLys 62

QY 257 GCCAACGTTGACTACAGAGATCGTGGTGACACCTCGAGGACCAATCGGCTGCTCA 316
DB 63 AlaSerValAspTyrGluLysIleValArgAspThrCysArgGluIleGlyPheThrSer 82

QY 317 AACGATGTCGGACTTCATGCTCAACATCGAAGTCTTGTAAACATTGAGCAGAGAGC 376
DB 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnSer 102

QY 377 CCTGATATTGCCAGGGTGTGACCGCCACCTTACCAGAGAGCCGAGGAAATCGGTCT 436
DB 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAla 122

QY 437 GGAGACCGGGTCAATGTTGGCTATGCCAGGACGAAACCCAGAAATGATGCAATG 496
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Db 123 GlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142
QY 497 AGTCATGTTCTTGCACAACTCAAACTCGGTGCTCTCACCAGAGGTTCCGCAAGACGAAACC 556
Db 143 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAspGlyThr 162
QY 557 TCCCATGTTGAGCGCTGATCGGAAACCCAAAGTACTGTTGAGTATTACATGACAAC 616
Db 163 CysAlaTrpLeuArgProAspSerLysThrGlnValThrValGluTyrValAsnGluGly 182
QY 617 GGTGCCATGTTCCAGTTCGTCTCCACACTGCTTATCTCCACCAACCAATGATGAGACT 676
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202
QY 677 GTGACCAACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCG 736
Db 203 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222
QY 737 GAGAACTACCTTGATGAGAGAACCACTTTTCCACTTGAACCCCTCTGGCCGCTTTGTCATT 796
Db 223 GluArgTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIle 242
QY 797 GGAGGTCTCTCAGGTGATGCTGCTCACCAGCCGCAAGATCATCATCGATACCTACGGA 856
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 262
QY 857 GGATGGGTGCTCATGCTGGTGGTCTTTCTCCGGGAAGGATCCCAACCAAGGTTGATAGG 916
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282
QY 917 AGTGTGTTTACATTGTGAGACAGCTGCTAAGAGCATTGTGGCAAGTGGACTAGCCAGA 976
Db 283 SerGlyAlaTyrValAlaArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 302
QY 977 AGGTGCATTGCAAGTGTCTTATGCCATTGGTGGCCGAGCCTTGTGCTGCTTGT 1036
Db 303 ArgCysLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322
QY 1037 GACACTATGGCACCGGGAAGATCCATGATAGGAGATTCTCAACATGTTGAAGGAGAAC 1096
Db 323 AspSerTyrGlyThrGlyThrIleProAspLysGluIleLeuLysIleValLysGluAsn 342
QY 1097 TTTGATTTTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156
Db 343 PheAspPheArgProGlyMetValThrIleAsnLeuAspLeuLysLysGlyGly---Asn 361
QY 1157 AGGTTCTTCAGACTGCTGCATATGCACATCTCGCAGAGAGCCCTGACTTCATCGG 1216
Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrp 381
QY 1217 GAAGTGGTCAAGCCCTCAAG 1237
Db 382 GluValValLysProLeuLys 388

RESULT 8
AAW34542
ID AAW34542 standard; protein; 394 AA.
XX
AC AAW34542;
XX
DT 26-MAR-1998 (first entry)
XX
DE S-adenosylmethionine synthase 3.
XX
KW S-adenosylmethionine synthase 3; sam3; barley; alkali resistant plant.
XX
OS Hordeum vulgare.
XX
PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-00133406.
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XX 28-MAY-1996; 96JP-00133406.
XX (NIOC ) NIPPON OIL CO LTD.
XX WPI; 1998-080077/08.
XX N-PSDB; AAT99143.
XX S-adenosyl-methionine synthase gene - useful in producing plants
PT resistant to alkaline soil.
XX Claim 3; Page 7-8; 13pp; Japanese.
XX This sequence represents the S-adenosylmethionine synthase 3 (sam3)
CC protein. The DNA encoding this sequence may be used in producing plants
CC which are resistant to alkaline soil
XX Sequence 394 AA;
SQ
Alignment Scores:
Pred. No.: 1,78e-182 Length: 394
Score: 1900.50 Matches: 354
Percent Similarity: 96.16% Conservative: 22
Best Local Similarity: 90.54% Mismatches: 14
Query Match: 69.16% Indels: 1
DB: 2 Gaps: 1
US-10-734-698A-38 (1-1485) x AAW34542 (1-394)
QY 77 GCAGAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAGCTCTGC 136
Db 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCy8 22
QY 137 GACCAAAATCTCGATGCTGCTCCTCGACGCTTCCCTTGAACAGAGCCACGACAGCAAGTTT 196
Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal 42
QY 197 GCTCGGAAACATGCACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCCACCAAG 256
Db 43 AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLys 62
QY 257 GCCAACGTTGACTTACGAGAGATCGTGCCTGACACCTCGAGGAACATCGCTTCTCTCA 316
Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAspIleGlyPheIleSer 82
QY 317 AACGATGCGGACTTGATCTGACAACTGCAAGTCTCTTGTAAACATTCAGCAGCAGAC 376
Db 83 AspAspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnSer 102
QY 377 CCTGATATTGCCAGGCTGTCACGGCCACCTTACCAGGAGACCCGAGGAATCGTGCT 436
Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122
QY 437 GGAGACAGGGTGCATGTTGGCTATGCGCAGGACGAAACCCAGAAATTCATGTCATTG 496
Db 123 GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142
QY 497 AGTCATGTTCTTGCAACTAACTCGGTGCTGCTCCTCACCAGGTTCCGAAAGCAAGACC 556
Db 143 ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162
QY 557 TGCCCATGTTGAGGCTCATGGGAAACCCAGTGACTGTTGAGTATTACATGACAAAC 616
Db 163 CysAlaThrLeuArgProAspGlyLysThrGlnValThrIleGluThrLeuAsnGluGly 182
QY 617 GTTGCCATGTTCTGCTGCTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGCT 676
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202
QY 677 GTGACCAACGACGAAATTCAGCTGACCTCAGGAGCATGTGATCAAGCCGGTGTCCGG 736
Db 203 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222

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QY 737 GAGAAGTACCTTGATGAGAACACCATTTTCCACTTGTAAACCCCTCTGGCCGCTTTGTTCATT 796
Db 223 GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242
QY 797 GGAGGTCTCCTACGGTGATGCTGGTCTCACCGCCGCGCAAGATCATCATCTTACCGGA 856
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 262
QY 857 GGATGGGTGCTCATGTTGGTGGTCTTCTCCCGGAGGATCCACCAAGCTTGATAGG 916
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282
QY 917 AGTGGTCTTACATTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTAGCCAGA 976
Db 283 SerGlyAlaTyrIleAlaArgGlnAlaLysSerIleIleAlaSerGlyLeuAlaArg 302
QY 977 AGTGCAATGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTGTCTGTCTTTGTT 1036
Db 303 ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322
QY 1037 GACACCTATGCGACCGGGAAGATCCATGATAAGAGATTTCTCAACATTTGTGAAGGAGAAC 1096
Db 323 AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAsn 342
QY 1097 TTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156
Db 343 PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysGlyGly--Lys 361
QY 1157 AGGTTCTTGAAGACTGCTGCATATGGACATCTTCGGCAGAGAGGACCTTGATTCACATGG 1216
Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381
QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249
Db 382 GluValValLysProLeuLysPheAspLysAla 392
RESULT 9
AAW34540
ID AAW34540 standard; protein; 394 AA.
XX AC AAW34540;
XX DT 26-MAR-1998 (first entry)
XX DE S-adenosylmethionine synthase 1.
XX KW S-adenosylmethionine synthase 1; sam1; barley; alkali resistant plant.
XX OS Hordeum vulgare.
XX PN JP09313186-A.
XX PD 09-DEC-1997.
XX PF 28-MAY-1996; 96JP-00133406.
XX PR 28-MAY-1996; 96JP-00133406.
XX PA (NIOC ) NIPPON OIL CO LTD.
XX DR WPI; 1998-080077/08.
XX N-PSDB; AAT99141.
XX S-adenosyl-methionine synthase gene - useful in producing plants
PT resistant to alkaline soil.
XX Claim 1; Page 5-6; 13pp; Japanese.
XX CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)
CC protein. The DNA encoding this sequence may be used in producing plants
CC which are resistant to alkaline soil
XX Sequence 394 AA;

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Alignment Scores:

Pred. No.: 1.78e-182 Length: 394  
Score: 1900.50 Matches: 354  
Percent Similarity: 96.16% Conservative: 22  
Best Local Similarity: 90.54% Mismatches: 14  
Query Match: 69.16% Indels: 1  
DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW34540 (1-394)

QY	77	GCAGAGACATTCCTATTACCTCAGAGTCAAGAGGAGACACCTGACAGCTCTGC	136
DB	3	AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys	22
QY	137	GACCAATCTCCCATGCTGCTCGACGCTTGCTTGAACAGGACCCAGACACCAAGGTT	196
DB	23	AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal	42
QY	197	GCTGCGAACAATGCAACAGACAACTTGCTCATGCTTCGAGAGATCACCAAG	256
DB	43	AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLys	62
QY	257	GCCAACTGACATACAGAGATCGTCGTCACCTGACAGGACATCGCTTCGCTCA	316
DB	63	AlaThrValAspTyrGluLysIleValArgAspThrCysArgAspIleGlyPheIleSer	82
QY	317	AACGATGTGGCACTCATGCTGACAACTGCAAGTCTTGTAAACATTGACGACGAGC	376
DB	83	AspAspValGlyLeuaspAlaAspHisCysLysValLeuValAsnIleGluGlnSer	102
QY	377	CCTGATATTGCCAGGTTGTCACGCGCACTTACCAGAGACCCGAGGAAATCGGTGCT	436
DB	103	ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluValGlyAla	122
QY	437	CGAGACAGGTCACATTTGCTATGCCAGGACGAAACCCAGCAATGTGCCATG	496
DB	123	GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu	142
QY	497	AGTCATGTTCTTCAACTAACTCGGTGCTCGCTCACCGAGGTTCCGCAAGAACGCC	556
DB	143	ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr	162
QY	557	TGCCCATGTGTAGGCTGATGGGAAACCCAAAGTCACTGTTGAGTATTACAATGACAAC	616
DB	163	CysAlaTrpLeuArgProAspGlyLysThrGlnValThrIleGluTyrLeuAsnGluGly	182
QY	617	GGTGCCATGTTCCAGTTCGTGCCACACTGTGCTTATCTCCACCCCAACATGATGACT	676
DB	183	GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr	202
QY	677	GTGACCAACGACGAAATTTGCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCG	736
DB	203	ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValLysProValIlePro	222
QY	737	GAGAATACCTTGATGAGAGACCAATTTCCACTTGAACCCCTCTCGCGCTTTTGTCAAT	796
DB	223	GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle	242
QY	797	GGAGTCTTCACGGTGATGCTGCTCACGGCGCGCAAGATCATCATCTACTTACGGA	856
DB	243	GlyGlyProHisGlyAspAlaGlyLeuThrAlaArgLysIleIleIleAspThrTyrGly	262
QY	857	GGATGGGTGCTCATGCTGTGTGCTTCTCCCGGAAGGATCCCAACCAAGGTTGATAGG	916
DB	263	GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg	282
QY	917	AGTGTGCTTACATTTGACAGAGGCTGCTTAAGAGCATTTGTGGCAAGTGGACTAGCAGA	976
DB	283	SerGlyAlaTyrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg	302
QY	977	AGTGTGATTTGCAAGTGTCTTATGTCATTTGTGTCGCCGAGCTTTGTCTTTGTT	1036

DB	303	ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal	322
QY	1037	GACACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAAC	1096
DB	323	AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAsn	342
QY	1097	TTTGATTTCAGGCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC	1156
DB	343	PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysLysGlyGly---Asn	361
QY	1157	AGTTTCTTCAAGACATGCTGCATATGGACACTTTCGGCAGAGAGACCTCGACTTCACATGG	1216
DB	362	ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp	381
QY	1217	GAAGTGGTCAAGCCCTCAAGTGGGAGAGAGGCC	1249
DB	382	GluValValLysProLeuLysPheAspLysAla	392
RESULT 10			
ID	AAW97744 standard; protein; 394 AA.		
XX	AAW97744;		
XX	21-MAY-1999 (first entry)		
DE	Wheat S-adenosylmethionine synthetase.		
XX	S-Adenosylmethionine synthetase; wheat; amino acid; lysine; threonine;		
KW	methionine; cysteine; isoleucine; transgenic plant; crop improvement;		
KW	food; feedstuff.		
OS	Triticum aestivum.		
XX	Key Location/Qualifiers		
FT	Misc-difference 93	/note= "encoded by AAR"	
FT	Misc-difference 150	/note= "encoded by CTY"	
FT	Misc-difference 155	/note= "encoded by ACS"	
FT	Misc-difference 282	/note= "encoded by CGY"	
FT	Misc-difference 290	/note= "encoded by CAR"	
XX	WO9855601-A2.		
XX	10-DEC-1998.		
XX	05-JUN-1998; 98WO-US011692.		
PR	06-JUN-1997; 97US-0048771P.		
PR	12-JUN-1997; 97US-0049443P.		
XX	(DUPO ) DU PONT DE NEMOURS & CO E I.		
PI	Falco SC, Allen SM, Rafaleki JA, Hitz WD, Kinney AJ, Abell LM;		
PI	Thorpe CJ;		
XX	WPI; 1999-070263/06.		
DR	N-PSDB; AAX07185.		
XX	New plant amino acid biosynthetic enzymes, DNA and chimeric genes -		
PT	encode: dihydrodipicolinate reductase; diaminopimelate epimerase; threonine		
PT	synthase; threonine deaminase; S-adenosylmethionine synthetase.		
XX	Example 7; Page 70-71; 98pp; English.		
PS	This is the amino acid sequence of a full-length wheat S-		
CC	adenosylmethionine synthetase, as deduced from a cDNA contig (see		
CC	AAX07185) obtained from kernel, leaf, seedling and root cDNA clones. The		
CC	wheat enzyme shows sequence similarity to the barley enzyme. The		

CC invention relates to new isolated nucleic acid fragments (see AAX07168-  
 CC 85) encoding plant enzymes (see AAW97727-44) that catalyze steps in the  
 CC biosynthesis of lysine, threonine, methionine, cysteine and isoleucine  
 CC from aspartate, the enzyme being selected from dihydropicolinate  
 CC reductase, diaminopimelate epimerase, threonine synthase, threonine  
 CC deaminase or S-adenosylmethionine synthetase. The invention also relates  
 CC to the construction of a chimeric gene encoding all or a portion of the  
 CC biosynthetic pathway enzyme, in sense or antisense orientation, where  
 CC expression of the chimeric gene results in production of altered levels  
 CC of the enzyme in a transformed host cell. Overexpression or reduction of  
 CC expression of genes encoding the amino acid biosynthetic pathway enzymes  
 CC in crop plants such as corn, soybean and wheat can be used to alter  
 CC levels of the amino acids in human food and animal feed. Transformed host  
 CC cells can also be used to identify compounds that inhibit one of the  
 CC enzymes

XX Sequence 394 AA;

Alignment Scores:  
 Pred. No.: 1,45e-181 Length: 394  
 Score: 1891.50 Matches: 355  
 Percent Similarity: 95.40% Conservatives: 18  
 Best Local Similarity: 90.79% Mismatches: 17  
 Query Match: 68.83% Indels: 1  
 DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW97744 (1-394)

QY 77 GCAGAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGC 136  
 Db 3 AlaGluThr-PheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22  
 QY 137 GACCAATCTCGAGTCTGCTCGACGCTTGCCCTGGAACAGGACCCAGACGAGGTT 196  
 Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaAspSerLysVal 42  
 QY 197 GCTCGGAAACATGACACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCAACCAAG 256  
 Db 43 AlaCysGluThrValThrLysThrAsnMetValMetValLeuGlyGluIleThrThrLys 62  
 QY 257 GCCAACGTTGACTACGAGAGATCGTGGTGAACCTGCGTGAACATCGGCTTCGTCTCA 316  
 Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSer 82  
 QY 317 AACGATGTGGACTGCTGCACTGCAACTCGAGGTCCTTGTAAACATTCAGCAGCAGAC 376  
 Db 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGlnGlnSer 102  
 QY 377 CCTGATATTGCCAGGGTGTGCACGGCCACCTTACCAGGACCCGAGGAAATCGGTGCT 436  
 Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122  
 QY 437 GGAGACAGGGTCACATTTTGGCTATGCCAGGACGAAACCCAGAAATTCATGTCATTTG 496  
 Db 123 GlyAspGlnGlyMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142  
 QY 497 AGTCATGTTCTGCACTAACTCGGTGCTGCTCACCAGGTTCCGAGAACCGGAC 556  
 Db 143 LysHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162  
 QY 557 TGCCCATGTTGAGGCTCATGGGAAACCCCAAGTGACTGTTGAGTATTACATACCAAC 616  
 Db 163 CysAlaTrpValArgProAspGlyLysThrGlnValThrValGluTyrLeuAsnGluAsp 182  
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 Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202  
 QY 677 GTGACCAACGACGAATTCAGTGTGACCTCAGGACGATGTCATCAGCGGTGATCCCG 736  
 Db 203 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222  
 QY 737 GAGAAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGGCCGTTTGTGCTATT 796

Db 223 AlaLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242  
 QY 797 GGAGGTCTCTACGGTGTGCTGCTCACCAGGCGCAGATCATCATCATCTTACCGA 856  
 Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGly 262  
 QY 857 GGATGGGGTCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACAAAGTTTCATAGG 916  
 Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282  
 QY 917 AGTGTGCTTACATTTGTGAGACAGCGCTCTAAGAGCATTGTGGCAAGTGGACTAGCCAGA 976  
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 QY 1097 TTTGATTTTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATAAC 1156  
 Db 343 PheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysLysGlyGly---Asn 361  
 QY 1157 AGGTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGCCCTGACTTCACATGG 1216  
 Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381  
 QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 382 GluValValLysProLeuLysPheAspLysAla 392  
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 AAW34541  
 ID AAW34541 standard; protein; 394 AA.  
 XX AC AAW34541;  
 XX DT 26-MAR-1998 (first entry)  
 XX DE S-adenosylmethionine synthase 2.  
 XX KW S-adenosylmethionine synthase 2; sam2; barley; alkali resistant plant.  
 XX OS Hordeum vulgare.  
 XX PN JP093113186-A.  
 XX PD 09-DEC-1997.  
 XX PF 28-MAY-1996; 96JP-00133406.  
 XX PR 28-MAY-1996; 96JP-00133406.  
 XX PA (NIOC ) NIPPON OIL CO LTD.  
 XX DR WPI; 1998-080077/08.  
 XX DR N-PSDB; AAT99142.  
 XX PT S-adenosyl-methionine synthase gene - useful in producing plants  
 PT resistant to alkaline soil.  
 XX Claim 2; Page 6-7; 13pp; Japanese.  
 CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)  
 CC protein. The DNA encoding this sequence may be used in producing plants  
 CC which are resistant to alkaline soil  
 XX Sequence 394 AA;

## Alignment Scores:

Pred. No.: 4, 63e-181 Length: 394  
Score: 1886.50 Matches: 353  
Percent Similarity: 95.40% Conservative: 20  
Best Local Similarity: 90.28% Mismatches: 17  
Query Match: 68.65% Indels: 1  
DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW34541 (1-394)

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QY 137 GACCAATCTCCGATGCTGCTCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTT 196
DB 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaSerLysVal 42

QY 197 GCTGCGAAACATGCAACAGCAACATTCGTCATGGTCTTCGGAGAGATCACCAAG 256
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QY 257 GCCAAGCTTGACTACGAGAGATCGCTGACACCTGCAGGAAACATCGCTTCGTCTCA 316
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QY 317 AACGATGTGGACTTGATGCTGCAACTGCAAGTCTCTTGTAAACATTGAGCAGCAGAGC 376
DB 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnIleSer 102

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DB 143 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162

QY 557 TGCCCATGTTGAGGCTGATGGGAAACCCAAAGTGAATGTTGAGTATTCAATGACAAC 616
DB 163 CysAlaTrpValArgProAspGlyLysThrGlnValThrIleAsnThrLeuAsnGluAsp 182

QY 617 GGTGCCATGTTCCAGTCTGCTGCCACATGCTTATCTCCACCCCAACATGATGACT 676
DB 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202

QY 677 GTGACCAACGAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCG 736
DB 203 ValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIlePro 222

QY 737 GAGAATGACTTGATGAGAACCAATTTCCACTTGAAACCCCTCTGGCCGTTTGTTCATT 796
DB 223 AlaLysThrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242

QY 797 GGAGTCTCCAGGTCATGCTGCTCAGCGCCGCAAGATCATCATCATCTACGATACCGA 856
DB 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThrGly 262

QY 857 GGATGGGTGCTCATGGTGGTGTGCTTCTCCGGAAGGATCCCAACCAAGTTGATAGG 916
DB 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282

QY 917 AGTGGTCTTACATTTGAGACAGGCTGCTTAAGACCAATTTGGCAAGTGCAGTACCGAGA 976
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QY 1097 TTTGATTTTCAGGCCCCGATGATCTCCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156
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XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48341.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX
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Alignment Scores:				
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DB	34	ProAspLeuAspSerAsnLeuSerProSerLeuLeuProSerThrGluMet---GluThr	52	
QY	86	TTCTCTATTTCACCTCAGAGTCAGTGAACAGGGACACCTGCACAAAGCTCTGCGACCAATC	145	
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QY	146	TCCGATGCTGCTCTCGACGCTTCCCTTGAACAGGACCCAGACAGAGAGTTCCTCGGAA	205	
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QY	206	ACATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAAGGCCAAGCTT	265	
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QY	266	GACTACGAGAAATCGTGGCTGCACCTCGCAGAAACATCGGCTTCGTCTCAACACGATGTG	325	
DB	113	AspTyrGluLysIleValArgSerThrCysArgGluIleGlyPheIleSerAlaAspVal	132	
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DB	133	GlyLeuAspAlaAspIleCysAsnValLeuValAsnIleGluGlnGlnSerProAspIle	152	
QY	386	GCCAGGGTGTGCACGGCCACTTACCAAGACCCGAGGAATCGTCTCGAGACCCAG	445	
DB	153	AlaGlnGlyValHisGlyHisLeuThrLysLeuProGluAspIleGlyAlaGlyAspGln	172	
QY	446	GGTCACATGTTTGGCTATGCCAGCGAAGAACCCAGAAATTGATGCTTTCATGATGTT	505	
DB	173	GlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThrHisVal	192	
QY	506	CTTGCAACTAACTCGGTGCTCTCACCAGGTTTCGCAAGAACCGAACCTGCGCCATGG	565	
DB	193	LeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCysProTrp	212	
QY	566	TTGAGGCTGATCGGAAACCCAGTGACTGTTGAGTATTACATCAACACCGTGCATG	625	
DB	213	LeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspGlyGlyAlaMet	232	
QY	626	GTTCACAGTTCGTGCACACTGTGCTATCTCCACCAACATCATGAGACTGTGACCAAC	685	
DB	233	IleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsn	252	
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QY	746	CTTGATGAGNAGACCAATTTCCACTTGAACCCCTCTGGCGGTTTCTCATTTGGAGTCT	805	
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QY	1166	AAGACTGTGCATATGGACATTCGCGCAGAGAGGACCTTGACTTCACATGGGAAGTGGTC	1225
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX	Arabidopsis thaliana.		
OS	Arabidopsis thaliana.		
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Alignment Scores:
Pred. No.: 1,35e-179 Length: 390
Score: 1872.00 Matches: 348
Percent Similarity: 95.08% Conservative: 19
Best Local Similarity: 90.16% Mismatches: 19
Query Match: 68.12% Indels: 0
DB: 3 Gaps: 0

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QY 140 CAAATCTCCGATGCTCTCTGACGCTTGCCTTGAACAGAGACCCAGAGAGTGGC 199
DB 22 GinIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
QY 200 TCGGAACATGACACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCCACCAAGGCC 259
DB 42 CysGluThrCysThrLysThrAsnMetValPheGlyGluIleThrThrAlaAla 61
QY 260 AAGCTTGACTACGAGAAAGATCGTGGTGCACCTGACGAGAAACATCGCTTCTCAAC 319
DB 62 LysValAspTyrGluLysIleValArgSerThrCysArgGluIleGlyPheIleSerAla 81
QY 320 GATGTGGGACTGATCTGACAACTCAAGCTCTTGTAAACATTGAGCAGAGACCTCT 379
DB 82 AspValGlyLeuAspAlaAspLysCysAsnValLeuValAsnIleGluGlnSerPro 101
QY 380 GATATTGCCCGGTGTGACGGCCACCTTACCAAGACCCGAGGAATCGGTCTGGA 439
DB 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluAspIleGlyAlaGly 121
QY 440 GACACGGGTACATGTTTGGCTATGCGACGAGAAACCCAGAAATTTGATGCTTGGT 499
DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCACAACTCCGCTGCTCTCACCGAGGTTGCGAAGAACCGAACCTGTC 559
DB 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCys 161
QY 560 CCATGGTTGAGCCCTGATCGGAACCCAGTCACTGTTGAGTATTACATCAACAGGT 619
DB 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspGlyGly 181
QY 620 GCATGTTTCCGATCGTGTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGG 679
DB 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAACGACGAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG 739
DB 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProAla 221
QY 740 AGTACCTTGATGAGAGACCAATTTCCACTTGAACCCCTCTGGCGGTTTGTGATTGGA 799
DB 222 LysTyrLeuAspAspAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTCAGGTCATGCTGCTCTCACCGCGCCGCAAGATCATCATGATATTACGAGGA 859
DB 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleIleIleIleIleIle 261
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QY 980 TGCATTGTGCAAGTCTCTTATGCCATTTGGTGTGCCGAGCCCTTGTCTGTCTTGTGAC 1039
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QY 1160 TTCTTGAAGACTGTGTCATATGGACATTCGCGACAGAGACCCCTGACTTTCATCGGAA 1219
DB 362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381
QY 1220 GTGGTCAAGCCCTCAAG 1237
DB 382 ValValLysProLeuLys 387

RESULT 14
AAY72078
ID AAY72078 standard; protein; 390 AA.
XX AAY72078;
XX 28-MAR-2001 (first entry)
XX Nicotiana tabacum S-adenosylmethionine synthetase (SAMS).
XX Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
XX herbicide resistance; S-adenosylmethionine synthetase; SAMS.
XX Nicotiana tabacum.
XX WO200067558-A1.
XX 16-NOV-2000.
XX 05-MAY-2000; 2000WO-US012450.
XX 06-MAY-1999; 99US-0132919P.
XX (TIMK/) TIMKO M.
XX Timko M;
XX WPI; 2001-007279/01.
XX N-PSDB; AAD02296.
XX New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
XX e.g. for producing transgenic plants with altered nicotine content.
XX Claim 17; Page 79-81; 103pp; English.
XX The invention relates to enzymes involved in alkaloid, specifically
XX nicotine, synthesis in tobacco and nucleic acids encoding them. The
XX nucleic acid of the invention can be used, in sense or antisense
XX orientation, to produce transgenic tobacco plants with altered alkaloid
XX content, and also for expression of exogenous proteins, e.g.
XX pharmaceutical proteins or proteins implicated in resistance to
XX herbicides. The protein of the invention can be used to identify
XX modulators of enzymatic activity in plants. The present sequence is
XX Nicotiana tabacum S-adenosylmethionine synthetase (SAMS). This enzyme is
XX involved in the nicotine biosynthetic pathway
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SQ Sequence 390 AA;

**Alignment Scores:**

Pred. No.:	2,71e-179	Length:	390
Score:	1869.00	Matches:	348
Percent Similarity:	94.82%	Conservative:	18
Best Local Similarity:	90.16%	Mismatches:	20
Query Match:	68.01%	Indels:	0
DB:	4	Gaps:	0

US-10-734-698A-38 (1-1485) x AAY72078 (1-390)

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Qy	140	CAAAATCTCCGATGCTGCTCCGACGCTTGCTTCAACAGGACCCAGACACGACGATGGCC	199
Db	22	GlnValSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla	41
Qy	200	TGCCAAATCATGCAACAAAGACCAACTTGGTTCATGCTTTCGAGAGATCACACCAAGGCC	259
Db	42	CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla	61
Qy	260	AACGTTGACTACGAGAAGATCGTGCGTGACACCTGCAGGAACATCGGCTCGTCTCAAC	319
Db	62	ThrValAspTyrGluLysIleValArgAspThrCysArgGlyIleGlyPheThrSerAla	81
Qy	320	GATGTGGGACTTGATGCTGACAACTGCAAGTCTCTGTTAAACATTTGACGACGAGCCCT	379
Db	82	AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro	101
Qy	380	GATATTGCCAGGCTGTGCACGGCCACTTACCAAAAGACCCGAGGAAATCGGTCTGGGA	439
Db	102	AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyValGly	121
Qy	440	GACCAGGTCACATGTTTGGCTATGCCACGGACGAAACCCGAGAAATTGATGCCATTGAGT	499
Db	122	AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr	141
Qy	500	CATGTTCTTGCAACTTAACCTCGGTCTGCTCTCACCGAGGTTCGCAGAGACGGAACTGC	559
Db	142	HisValTrpAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCys	161
Qy	560	CCATGTTTGAGGCTGATGGGAAAACCCCAAGTGACTGTTGAGTATTACAATGACAAACGGT	619
Db	162	ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspAsnGly	181
Qy	620	GCCATGTTTCCAGTTCGTGTCACACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTG	679
Db	182	AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal	201
Qy	680	ACCAACGACGAAATTCGACGTGACTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAG	739
Db	202	ThrAsnAspGlnIleAlaGlnAspLeuLysGluHisValIleLysProValIleProSer	221
Qy	740	AAGTACCTTGATGAGAACCATTTCACACTTGAACCCCTCTGCGCGTTTGTTCATTTGGA	799
Db	222	GlnTrpLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly	241
Qy	800	GGTCCTCACGGTGTATGCTGCTCTCACCGGCGCAGATCATCATCGATCTTACGAGGA	859
Db	242	GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly	261
Qy	860	TGGGGTGCTCATGTGTGTGTGCTTTCTTCGGGAAGGATCCCAACAGTTGATAGAGT	919
Db	262	TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer	281
Qy	920	GGTCGCTTACATTGTGACACGGCTCTAAGAGCATTTGTGGCAAGTGCAGCTAGCCAGAGG	979
Db	282	GlyAlaTyrIleValArgGlnAlaLysSerValValAlaSerGlyLeuAlaArgArg	301
Qy	980	TGCATTGTGCAAGTGTCTTATGCAATCTGGTGTGCGCGAGCCCTTGTCTGTCTTTGTTCAC	1039

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US-10-734-698A-38 (1-1485) x AAG40367 (1-344)

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1946	70.8	396	4	US-09-424-978B-36 Sequence 36, Appl
3	1891.5	68.8	394	4	US-09-424-978B-42 Sequence 42, Appl
4	1317	47.9	416	4	US-09-949-016-10059 Sequence 10059, A
5	1316.5	47.9	395	4	US-09-976-594-471 Sequence 471, Appl
6	1280.5	46.6	390	4	US-09-248-796A-18255 Sequence 18255, A
7	1274.5	46.4	395	4	US-09-949-016-5939 Sequence 5939, Ap
8	1274.5	46.4	401	4	US-09-949-016-7658 Sequence 7658, Ap
9	1103	40.1	404	4	US-09-107-532A-6821 Sequence 6821, Ap
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11	1068.5	38.9	385	4	US-09-489-039A-11917 Sequence 11917, A
12	1063.5	38.7	405	4	US-09-107-433-2830 Sequence 2830, Ap

13	1062.5	38.7	396	4	US-09-583-110-2778 Sequence 2778, Ap
14	1061.5	38.6	396	3	US-09-273-686-2 Sequence 2, Appl
15	1055	38.4	395	4	US-09-328-352-6660 Sequence 6660, Ap
16	1042.5	37.9	415	3	US-09-134-001C-5077 Sequence 5077, Ap
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19	1028.5	37.4	402	3	US-08-510-648B-20 Sequence 20, Appl
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#### ALIGNMENTS

##### RESULT 1

US-09-424-978B-39  
; Sequence 39, Application US/09424978B  
; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; CURRENT FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-424-978B-39

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US-10-734-698A-38 (1-1485) x US-09-424-978B-39 (1-392)

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; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; CURRENT FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/046,771  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
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; TYPE: PRT  
; ORGANISM: Zea mays  
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Db 245 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 264  
QY 860 TGGGGTCTCATGCTGCTGCTCTCTCCGGGAGGATCCCAAGGTTGATGAGACT 919  
Db 265 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 284  
QY 920 GTGCTTACATTTGTGAGACAGGCTGCTTAAGACATTTGTGGCAAGTGGACTAGCCAGG 979  
Db 285 GlyAlaTyrValAlaArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArg 304  
QY 980 TGCATTGTCAAGTCTTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039  
Db 305 AlaIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 324  
QY 1040 ACCTATGGCACCGGAGATCCATGATAGGACATTTCTCAACATTTGAGGAGACTTT 1099  
Db 325 ThrTyrGlyThrGlyAlaIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 344  
QY 1100 GATTTCAGGCGCGTATGATCTCCATCAACTTGATCTCAAGAGGGTGGGAATACAG 1159  
Db 345 AspPheArgProGlyMetIleIleLeuAsnLeuAspLeuLysGlyGlyAsnGlyArg 364  
QY 1160 TTCTTGAAGACTCTGCATATGACACTTGGCAGAGAGACCTTCATCTCATGCGGAA 1219  
Db 365 TyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 384  
QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAAG 1246  
Db 385 ValValLysProLeuLysSerGluLys 393

## RESULT 3

US-09-424-978B-42  
; Sequence 42, Application US/09424978B  
; Patent No. 666445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafaleki, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424, 978B  
; CURRENT FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048, 771  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 394  
; TYPE: PRT

; ORGANISM: Triticum aestiva  
US-09-424-978B-42

Alignment Scores:  
Pred. No.: 1-228-190 Length: 394  
Score: 1891.50 Matches: 355  
Percent Similarity: 95.40% Conservatives: 18  
Best Local Similarity: 90.79% Mismatches: 17  
Query Match: 68.83% Indels: 1  
DB: 4 Gaps: 1

US-10-734-698A-38 (1-1485) x US-09-424-978B-42 (1-394)

QY 77 GCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTCAAGCTCTGC 136  
Db 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22  
QY 137 GACCAAAATCTCCGATGCTGCTCTCCAGCTTCCCTTGAACAGGACCCAGACAGGTT 196  
Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaAspSerLysVal 42  
QY 197 GCCTGCGAAAACATGCACCAAGACCAACTTGGTCTCATGGTCTTCGAGAGATCAACCAAG 256  
Db 43 AlaCysGluThrValThrLysThrAsnMetValMetValLeuGlyGluIleThrLys 62  
QY 257 GCACACAGTTGACTACGAGAAGATCGTGGTGTGACACCTGCGAGAACATCGGTTCTCA 316  
Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSer 82  
QY 317 AACGATGGGAGCTTGTGCTGACAACTGCAAGGTCCTTGTAAACATGAGCAGCAGAGC 376  
Db 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnSer 102  
QY 377 CCTGATATTCACGAGTGTGACCGCCACCTTACCAAGACCCGAGGAAATCGGTCT 436  
Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122  
QY 437 GCAGACACAGGTCACATGTTGGCTATGCGACGACGAAACCCCAAGATTTGATGCCATTG 496  
Db 123 GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142  
QY 497 AGTCATGTTTGCATTAACCTCGGTCGTCTCACCGAGGTCGCAAGACCGAACCC 556  
Db 143 LysHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162  
QY 557 TGCCCATGTTGAGGCTGTGAGGAAACCCCAAGGACTGTTGAGTATTACATGACAC 616  
Db 163 CysAlaTrpValArgProAspGlyLysThrGlnValThrValGluThrLeuAsnGluAsp 182  
QY 617 GGTGCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACT 676  
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202  
QY 677 GTGACCAACGAGAAATTCAGCTGACCTCAAGAGCATGTGATCAAGCGGTGATGCCG 736  
Db 203 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222  
QY 737 GAGAAGTACCTTGATGAGAGACCACTTTCCACTTGAACCCCTCGCGGTTTTCTCAT 796  
Db 223 AlaLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242  
QY 797 GGAGGTCTCTCAGCGTGTGCTGCTCACCAGCGCCCAAGATCATCATGATATTACGGA 856  
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 262  
QY 857 GGATGGGTGCTCATGGTGGTGGTCTTCTCCCGGAAAGGATCCCAAGGTTGATAGG 916  
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282  
QY 917 AGTGTGCTTACATTTGTGAGACAGGCTGCTAAGACATTTGGGCAAGTGGACTAGCCAG 976  
Db 283 SerGlyAlaTyrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg 302



; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCES: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 471  
; LENGTH: 395  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6673549 2600262CD1  
US-09-976-594-471

Alignment Scores:  
Pred. No.: 7,14e-130 Length: 395  
Score: 1316.50 Matches: 254  
Percent Similarity: 78.50% Conservatives: 49  
Best Local Similarity: 65.80% Mismatches: 76  
Query Match: 47.91% Indels: 7  
DB: 4 Gaps: 3

US-10-734-698A-38 (1-1485) x US-09-976-594-471 (1-395)

QY 83 ACATTCTCTTTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGCGACCAA 142  
DB 17 ThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAspGln 36  
QY 143 ATCTCCGATGCTCTCTCGACGCTTGCCTTTGAACAGGACCCAGACAGAGGTTCCTGTC 202  
DB 37 IleSerAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValAlaCys 56  
QY 203 GAACATGACCAAGACCACTTGCTGTCATGCTTCGGAGAGATCAACCAAGGCCAAC 262  
DB 57 GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla 76  
QY 263 GTTGACTACGAGAGATCGCTGTGACACCTGACGAGCAACATCGCTTCTCTCAACAGAT 322  
DB 77 ValAspGlyGlnLysValValArgGluAlaValLysHisIleGlyTyrAspSerSer 96  
QY 323 GTGGGACTTGATGCTGACAACTGCAAGTCTTGTAAACATTCAGCAGCAGAGCCCTGAT 382  
DB 97 LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnSerProAsp 116  
QY 383 ATGCCCCAGGTGTGACGGCCACCTTACCAAGACCCGAGAAATCGGTGCTGGAGAC 442  
DB 117 IleAlaGlnGlyVal-----HisLeuAspArgAsnGluGluAspIleGlyAlaGlyAsp 134  
QY 443 CAGGTCACATGTTTGGCTATGTCACGAGCAACCCAGAAATTCATTCATTCATTCAT 502  
DB 135 GlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluGluCysMetProLeuThrIle 154  
QY 503 GTTCTTGCAACTAACTCGGTGCTCTCACGAGGTTCGCAAGAACGGAACCTGCCCA 562  
DB 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174  
QY 563 TGGTTGAGGCTGATGGGAAACCCCAAGTACCTGTTGAGTATTACATGACACCGTGGC 622  
DB 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194  
QY 623 ATGTTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACATGATGAGCTGTGACC 682  
DB 195 ValLeuProIleArgValHisThrIleValIleSerValGlnHisAspGluGluValCys 214  
QY 683 AACGCAAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCGGAGAAG 742  
DB 215 LeuAspGluMetArgAspAlaLeuLysGluLysValIleLysAlaValValProAlaLys 234  
QY 743 TACCTTGATGAGAAACCAATTTCCACTTGAAACCCCTCTGGCGGTTTGTCAATTGAGGT 802

DB 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254  
QY 803 CCTCAGCGTGATGCTCGTCTCACCGCCGCAAGATCATCATCGATATTACGAGGATGG 862  
DB 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleIleValAspThrTyrGlyGlyTrp 274  
QY 863 GGTGCTCATGCTGCTGCTTCTCCGGGAAGATCCCAACAGGTTGATGAGGATGGT 922  
DB 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294  
QY 923 GCTTACATTGTGACAGCGCTCTAAGACATTGTGGCAAGTGGAGTACCGAAGGTGC 982  
DB 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLeuCysArgArgVal 314  
QY 983 ATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCTTTGTCTGCTCTTGTGTGACAC 1042  
DB 315 LeuValGlnValSerTyrAlaIleGlyValSerHisProLeuSerIleSerIlePheHis 334  
QY 1043 TATGGCACCGGAAGATCCATGATAGGAGATTCTCAACATTGTGAGGAGAACTTTGAT 1102  
DB 335 TyrGlyThrSerGlnLysSerGluArgGluLeuLeuGluIleValLysLysAsnPheAsp 354  
QY 1103 TTCAGGCCGCTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATAACAGGTT 1162  
DB 355 LeuArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProIleTyr 371  
QY 1163 TTGAAGACTGCTGCATATGCACACTTCGGCAGAGAGACCCCTGACTTCACATGGGAAGTG 1222  
DB 372 GlnArgThrAlaAlaTyrGlyHisPheGlyArgAsp-----SerPheProTrpGluVal 389  
QY 1223 GTCAAGCCCTCAAGTGG 1240  
DB 390 ProLysLysLeuLysTyr 395

#### RESULT 6

US-09-248-796A-18255  
; Sequence 18255, Application US/09248796A  
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18255

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-18255

Alignment Scores:

Pred. No.: 4,51e-126 Length: 390  
Score: 1280.50 Matches: 242  
Percent Similarity: 77.00% Conservatives: 56  
Best Local Similarity: 62.53% Mismatches: 82  
Query Match: 46.60% Indels: 7  
DB: 4 Gaps: 3

US-10-734-698A-38 (1-1485) x US-09-248-796A-18255 (1-390)

QY 80 GAGACATTCTTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGCGAC 139  
DB 11 GluThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAsp 30  
QY 140 CAAATCTCGATGCTGCTCTCGACCTTCCTTGAACAGGACCCAGACAGGAGTGGC 199  
DB 31 GlnValSerAspAlaIleLeuAspAlaCysLeuAlaValAspProLeuSerLysValAla 50





Db	362	ArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProlleTyGln	378
Qy	1166	AAGACTGCTCATATGGACATCTTCGGCAGAGAGAGACCTGACTTCACATGGGAAGTGGTC	1225
Db	379	LysThrAlaCysTyGlyHisPheGlyArgSer-----GluPheProTrpGluValPro	396
Qy	1226	AAGCCCTC	1234
Db	397	ArgLysLeu	399
RESULT 9			
US-09-107-532A-6821			
; Sequence 6821, Application US/09107532A			
; Patent No. 6583275			
; GENERAL INFORMATION:			
; APPLICANT: Lynn A Doucette-Stamm and David Bush			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO			
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS			
; NUMBER OF SEQUENCES: 7310			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION			
; STREET: 100 Beaver Street			
; CITY: Waltham			
; STATE: Massachusetts			
; COUNTRY: USA			
; ZIP: 02354			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: CD-ROM ISO9660			
; COMPUTER: PC			
; OPERATING SYSTEM: <Unknown>			
; SOFTWARE: ASCII			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/107,532A			
; FILING DATE: 30-Jun-1998			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 60/085,598			
; FILING DATE: 14 May 1998			
; APPLICATION NUMBER: 60/051571			
; FILING DATE: July 2, 1997			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Ariniello, Pamela Deneke			
; REGISTRATION NUMBER: 40,489			
; REFERENCE/DOCKET NUMBER: GTC-012			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (781)893-5007			
; TELEFAX: (781)893-8277			
; INFORMATION FOR SEQ ID NO: 6821:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 404 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; HYPOTHETICAL: YES			
; ORIGINAL SOURCE:			
; ORGANISM: Enterococcus faecium			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (B) LOCATION 1...404			
; SEQUENCE DESCRIPTION: SEQ ID NO: 6821:			
US-09-107-532A-6821			
Alignment Scores:			
Pred. No.: 2.65e-107 Length: 404			
Score: 1103.00 Matches: 224			
Percent Similarity: 72.45% Conservative: 60			
Best Local Similarity: 57.14% Mismatches: 94			
Query Match: 40.14% Indels: 14			
DB: 4 Gaps: 5			
US-10-734-698A-38 (1-1485) x US-09-107-532A-6821 (1-404)			
Qy	68	ATTAAGATGCGAGAGACATTCCTATTTCCTCAGAGTCAGTGAACGAGGACACCCCTGAC	127

Db	181	-----IleValGlyIleAspAlaValValLeuSerThrGlnHisAlaGluAspIleSer	198
Qy	683	AACGACGAATTCGACGTGACCTCAAGGACGATGATCAAGCCGGTGATCCCGGAGAAG	742
Db	199	GlnLysAspLeuHisGluAlaValMetGluGluIleIleLysProIleLeuProThrGlu	218
Qy	743	TACCTTTGATGAGAAGACCAATTTTCCACTTTGAACCCCTCTGGCCGTTTGTTCATTGGAGGT	802
Db	219	TrpLeuAsnGluGlnThrLysTyrPheIleAsnProThrGlyArgPheValIleGlyGly	238
Qy	803	CCTCAGCGTGATGCTGCTCACCAGCGCCGACAGATCATCATCATATCATTACGAGAGATGG	862
Db	239	PrometGlyAspCysGlyLeuThrGlyArgLysIleIleValAspThrTyrGlyGlyMet	258
Qy	863	GGTGCTCATGGTGGTGGTCTTCTCCGGGAAGATCCCAACCAAGGTTGATAGGAGTGGT	922
Db	259	AlaArgHisGlyGlyAlaPheSerGlyLysAspProSerLysValAspArgSerAla	278
Qy	923	GCTTACATTTGTGACAGCGGTGCTAAAGAGCATTTGTGGCAAGTGGCATGAGCAGCAAGGTGC	982
Db	279	AlaTyrAlaAlaArgTyrValAlaLysAsnIleValAlaAlaGlyLeuAlaAspArgCys	298
Qy	983	ATTGTGCAAGTGCTTATGTCATTTGGTGTGTCGCCGAGCGCTTGTCTGCTTTGTGTGACACC	1042
Db	299	GluIleGlnValSerTyrAlaIleGlyValAlaGluProThrSerIleMetValGluThr	318
Qy	1043	TATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTCTGAAGGAGAAGCTTTTGTAT	1102
Db	319	PheGlyThrGlnLysIleProThrSerGlnLeuIleLeuLeuValArgGluPhePheAsp	338
Qy	1103	TTCAGGCCCC---GGTATGATCTCCATCAACCTTTGATCTCAAGAGGGGTGGGAATAACAGG	1159
Db	339	LeuArgProTyrGlyLeuIleGlnMet---LeuAspLeuLeu-----HisProIle	354
Qy	1160	TTCTTGAAGACTGCTGCATATGAGACATCTCGGCAGAGAGACCCTGACTTTCATCATGGGAA	1219
Db	355	TyrGlnLysThrAlaAlaTyrGlyHisPheGlyArg-----AlaGluPheProTyrGlu	372

RESULT 11

US-09-489-039A-11917

; Sequence 11917, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLBBS

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 11917

; LENGTH: 385

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11917

Alignment Scores:	
Pred. No.:	1,13E-103
Score:	1068.50
Percent Similarity:	71.39%
Best Local Similarity:	57.47%
Query Match:	38.88%
DB:	4
	Gaps: 8
	Length: 385
	Matches: 223
	Conservative: 54
	Mismatches: 92
	Indels: 19
	Gaps: 8

US-10-734-698A-38 (1-1485) x US-09-489-039A-11917 (1-385)

Qy	89	CTATTACTCAGACTGACGTGAACGGGACACCTTGACAGACTCTGCGACCAATCTCC	148
Db	6	LeuPheThrSerGluSerValSerGluGlyHisProAspLysIleAlaAspGlnIleSer	25

Qy	149	GATGCTGTCTTCGACGCTTGCTTGAACAGAGCCAGACACCAAGCAAGCTTGCTCTGCGAAACA	208
Db	26	AspAlaValIeuAaspAlaIleLeuGluGlnAaspProLysAlaAArgValAlaCysGluThr	45
Qy	209	TGCACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAGGACCAAGCTTGAC	268
Db	46	TyrValLysThrGlyMetValLeuValGlyGlyGluIleThrThrSerAlaIleThrValAsp	65
Qy	269	TACGAGAAGATCGTGCCTGCACCTCGCAGGAAACATTCGCTTCCTCAAAACGATGGCGGA	328
Db	66	IleGluGluIleThrArgAsnThrValArgGluIleGlyTyrValHisSerAaspMetGly	85
Qy	329	CTTGATGCTGAACACTCAAGGTCCTTGTAAACATTCAGCAGCAGACGCCCTGATATTGCC	388
Db	86	PheAspAlaAsnSerCysAlaValLeuSerAlaIleGlyLysGlnSerProAaspIleAsn	105
Qy	389	CAGGGTGTGCAGCGCCACCTTACCAAAGACCCGAGGAATCGGTGCTGAGACCAAGGT	448
Db	106	GlnGlyValAasp-----ArgAlaAaspProLeuGluGlnGlyAlaGlyAaspGlnGly	122
Qy	449	CACATGTTGGCTATGCCACGAGCAAAACCCAGAAATTGATGCTTCATTCAGTCATGTTCTT	508
Db	123	LeuMetPheGlyTyrAlaIleAsnGluThrAspValLeuMetProAlaProValThrTyr	142
Qy	509	GCAACTAAACTCGGTGCTGCTTCACCGAGGTTCGCAAGAACGGAACCTGCCCATGGTTG	568
Db	143	AlaHisArgLeuValGlnArgGlnAlaGluValArgLysAsnGlyThrLeuProTrioLeu	162
Qy	569	AGGCCTGATGGGAAACCCAAAGTCACTGTTGAGTATTACATGACACACGGTGCATGGTT	628
Db	163	ArgProAaspAlaLysSerGlnValThrPheGlnTyr-----AaspGlyLysIle--	179
Qy	629	CCAGTTCGTGTCACACTGTCCTTATCTCCACCCCAACATGATGATGATGATGATGATGAT	688
Db	180	---ValGlyIleAaspAlaValLeuIleAsnThrGlnHisAlaGluAaspIleAaspGlnLys	198
Qy	689	GAATATTCAGCTGACCTCAAGGAGCATGTGTATCAAGCCGGTGATCCCGGAGAAGTACCTT	748
Db	199	SerLeuGlnGluAlaValMetGluIleIleLysProIleLeuProThrGluTrioLeu	218
Qy	749	GATGAGAAGACCATTTCCACTTGAAACCCCTCTCGCGTTTGTTCATTTGAGGTCCCTCAC	808
Db	219	AsnAlaSerThrLysPheIleAaspProThrGlyArgPheValIleGlyGlyProMet	238
Qy	809	GGTGATGCTGCTCACCGCGCAAGATCATCATCTTACGAGAGATGGGGTCT	868
Db	239	GlyAaspCysGlyLeuThrGlyArgLysIleIleValAaspThrTyrGlyGlyMetAlaArg	258
Qy	869	CATGGTGTGTGCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGGTCTTAC	928
Db	259	HisGlyGlyGlyAlaPheSerGlyLysAaspProSerLysValAaspSerAlaIleTyr	278
Qy	929	ATTGTGACACAGGCTGTAAGACGATTTGTGCAAGTGGACTAGCCAGAGAGGTGATTTGTG	988
Db	279	AlaAlaArgTyrValAlaLysAsnIleValAlaAlaGlyLeuAlaAaspArgCysGluIle	298
Qy	989	CAAGTGTCTTATGCCATTGGTGTCCCGAGCCTTTGCTGCTTGTGTGTGACACCTTANGC	1048
Db	299	GlnValSerTyrAlaIleGlyValAlaGluProThrSerIleMetValGluThrPheGly	318
Qy	1049	ACCGGAAGATCCATGATTAAGGAGATTCTCAACATTTGTGAAGGAGAACTTTGATTTCCAGG	1108
Db	319	ThrGluLysValProSerGluGlnLeuThrLeuLeuValArgGluPheAaspLeuArg	338
Qy	1109	CCC---GGTATGATCTCCATCAACTTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTG	1165
Db	339	ProTyrGlyLeuIleGlnMet---LeuAaspLeuLeu-----HisProIleTyrLys	354
Qy	1166	AAGACTGCTGATATGGACATCTTCGGCAGAGAGGACCTGACTTTCACATGGGAAGTGGTC	1225
Db	355	GluThrAlaAlaTyrGlyHisPheGlyArgGlu-----HisPheProTrioLeu-----	370
Qy	1226	AAGCCCTCTCAAGTGGGGAAGGCC	1249

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Db          371  -----LythrAepLyAla 375
|||||
RESULT 12
US-09-107-433-2830
; Sequence 2830, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2830:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...405
; SEQUENCE DESCRIPTION: SEQ ID NO: 2830:
US-09-107-433-2830

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Score: 1063.50 Matches: 219
Percent Similarity: 70.66% Conservative: 58
Best Local Similarity: 55.87% Mismatches: 100
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DB: 4 Gaps: 5

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Qy	704	CTCAAGGAGCATGTGATCAACGCCGTGATCCCGGAGAGTACCTTGATGAGAAACACCAT	763
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RESULT 13

US-09-583-110-2778  
; Sequence 2778, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: P400-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 2778  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
; US-09-583-110-2778





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: August 25, 2005, 17:07:17 ; Search time 228 Seconds  
(without alignments)  
5118.381 Million cell updates/sec

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Searched: 1767149 seqs, 392926209 residues  
Total number of hits satisfying chosen parameters: 3534298

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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9	2149	78.2	423	15	US-10-425-114-55424 Sequence 45712, A
10	2149	78.2	423	15	US-10-425-114-55424 Sequence 45723, A
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35	2096	76.3	395	15	US-10-425-114-55424 Sequence 44212, A
36	2083	75.8	392	15	US-10-424-599-220046 Sequence 44833, A
37	2083	75.8	392	15	US-10-424-599-220046 Sequence 220046, A
38	2083	75.8	392	17	US-10-734-698A-39 Sequence 39, Appl
39	2062.5	75.1	393	15	US-10-424-599-220047 Sequence 220047, A
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44	2015.5	73.3	421	15	US-10-425-114-46219 Sequence 54713, A
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ALIGNMENTS

RESULT 1  
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; Sequence 55424, Application US/10425114  
; Publication NO. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Iau, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 55424  
; LENGTH: 421  
; TYPE: PRT

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; Sequence 51724, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
```

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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51724
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700961178_FLI.pep
US-10-425-114-51724
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Alignment Scores:
Pred. No.: 7,29e-193 Length: 421
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1
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US-10-734-698A-38 (1-1485) x US-10-425-114-51724 (1-421)

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QY 4 CAAGCCCACTCAACCCACACCACT-----CTCTCTGCTCTCTT 45
|
|
|
Db 1 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 20
|
|
|
QY 46 CTACCTTTCAAGTATTTAAAGTATTAAAGATGCGCAGAGCATTTCTTATTCTCAGAGTC 105
|
|
|
Db 20 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 40
|
|
|
QY 106 AGTGAAAGAGGACACCTCTGACCAAGCTCTGGACCAAAATCTCCGATGCTCTCGACGC 165
|
|
|
Db 40 rValAsnGluGlyHisProAspLysLeuLysAspGlnIleSerAspAlaValLeuAspAl 60
|
|
|
QY 166 TTGCTCTTGAACAGACGACCAAGCTTGCCTCGAAACATGSCACCAAGACCAACTT 225
|
|
|
Db 60 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 80
|
|
|
QY 226 GGTGATGCTCTTCGAGAGATCACCAAGCCCAAGCTTCACTACGAGAGATCGTCG 285
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|
Db 80 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 100
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|
QY 286 TGACACCTGCGAGGAACATCGCTTCGCTCAACAGATGTGGACTTGATGCTGCAACTG 345
|
|
|
Db 100 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 120
|
|
|
QY 346 CAAGTCCTCTTAAACATTGAGACGACGAGCCCTGATATTCCCAAGGTGTGACGGCCA 405
|
|
|
Db 120 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 140
|
|
|
QY 406 CTTTACCAAAAGACCCGAGGAAATCGGTGCTGGAGACCAAGGTCAATGTTTGGCTATGC 465
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|
|
Db 140 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 160
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|
|
QY 466 CACGACGAAACCCGAGAAATGATGCCATTGAGTCATGTTCTTCCAACTAAACTCGGTGC 525
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|
|
Db 160 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 180
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|
|
QY 526 TCGTCTCACCGAGGTTCCGAAAGACCGAACCTGCCCATGTTGAGGCTGTGATGGAAAC 585
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|
Db 180 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 200
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|
|
QY 586 CCAAGTGAAGTGTGAGTATTACAATGACAAACGGTGCCATGGTTCCAGTTCGTGTCCAC 645
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|
Db 200 rGlnValThrValGluThrValGluThrValGluThrValGluThrValGluThrVal 220
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|
|
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGTGACCAACGACGAATTCGACGTGAC 705
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|
|
Db 220 rValLeuLeuSerThrGlnHisAspGluThrValThrAsnAspGluThrValAlaAla 240
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|
QY 706 CAAGGAGCATGTGATCAAGCCCGTGATCCCGAGAGTACCTTGATGAGAGACCATTTT 765
|
|
|
Db 240 uLysGluHisValLysProValLysProValLysProValLysProValLysProVal 260
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|
|
QY 766 CCACCTGAACCCCTCTGGCCGTTTGTTCATTCGAGGTCTCAAGTGTGATGCTGCTT 825
|
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|
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Db 260 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 280  
QY 826 CGCCGCAAGATCATCATCTACTTACGAGAGATGGGGTCTCATGGTGGTCTT 885  
Db 280 rGlyArgLysIleIleIleAspThrTyGlyGlyTrpGlyAlaHisGlyGlyAlaPh 300  
QY 886 CTCGGGAAGATCCCAACCAAGTTGATAGAGTGGTCTTACATTGTGAGACAGCTGC 945  
Db 300 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyIleValArgGlnAlaI 320  
QY 946 TAAGAGATTGTGGCAAGTGCATAGCCAGAGGTGCATTGTCAGTGTCTTATGCCAT 1005  
Db 320 aLysSerIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyAlaI 340  
QY 1006 TGGTGTGCCGAGCTTTGTCTGTCTTTGTTCACCTATGGCACCAGGAGATCCATGA 1065  
Db 340 eGlyValProGluProLeuSerValPheValAspThrTyGlyThrGlyLysIleHis 360  
QY 1066 TAAGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTCAGCCCGGTATGATCTCCAT 1125  
Db 360 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerI 380  
QY 1126 CAACCTTGATCTCAAGAGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACA 1185  
Db 380 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyGlyH 400  
QY 1186 CTTCCGAGAGAGCCCTGACTTCATATGGGAGTGGTCAAGCCCTCAAGTGGGAGAA 1245  
Db 400 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGly 420  
QY 1246 GGCC 1249  
Db 420 sAla 421

## RESULT 5

US-10-425-114-71917  
; Sequence 71917, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 71917  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700751645\_FLI.pep  
US-10-425-114-71917

## Alignment Scores:

Pred. No.: 7,29e-193 Length: 421  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-71917 (1-421)

QY 4 CAAGCCCACTCAACACACACACCACT-----CTCTCTGCTCTTCTT 45  
Db 1 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyProPhe-LeuLeuPhePh 20  
|||||

QY 46 CTACCTTTCAAGTTTTTAAAGATTAAAGATGGCAGAGACATCTCTATTTACCTCAGATC 105  
Db 20 eTyLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 40  
QY 106 AGTGAACGAGGACACCCCTGACAAAGCTCTGCCACCAATCTCGGATCTGCTCTCAGCG 165  
Db 40 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 60  
QY 166 TTGGCTTTGAACAGGCCACAGCAAGGTTCCCTGCGAAACATGCACCAAGACCAACTT 225  
Db 60 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 80  
QY 226 GGTCTATGCTTCGAGAGATCACCAAGGCCAACGTTGACTACGAGAAGATCGTGGC 285  
Db 80 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 100  
QY 286 TCACACCTGCAGAAACATCGGCTTGTCTCAACAGATGGGACTGTGCTGACAACTG 345  
Db 100 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnC 120  
QY 346 CAAGGTCTCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCAGGGTGTGCACGCCA 405  
Db 120 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 140  
QY 406 CTTTACCAAAAGACCCGAGAAATCGGTGCTGAGACCAAGGCTCACATGTTTGGCTATGC 465  
Db 140 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyra 160  
QY 466 CACGACGAAACCCAGAAATTGATGCCATTGATGATGATGTTCTTGCACACTAAACTCGGTGC 525  
Db 160 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 180  
QY 526 TCGTCTCACCGAGGTTCCGAAGACCGAACCTGCCCATGTTGAGCCCTGATGGGAAAC 585  
Db 180 aArgLeuThrGluValAlaArgLysAsnGlyThrCysProThrLysLeuArgProAspGlyLysTh 200  
QY 586 CCAAGTGTGTTGAGTATTACAATGACAAACGCTGCCATGTTCCAGTTTCGTTGTCACAC 645  
Db 200 rGlnValThrValGluTyThrAsnAspAsnGlyAlaArgValProIleArgValHisTh 220  
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCGAGCTGACCT 705  
Db 220 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 240  
QY 706 CAAGGAGCATGTGATCAAGCGGTGATCCCGAGAGTACCTTGTGATGAGAAGACCATTTT 765  
Db 240 uLysGluHisValIleLysProValIleProGluLysTyLeuAspGluLysThrIlePh 260  
QY 766 CCACCTTGAACCCCTCTCGGCCGTTTTTGTTCATTGGAGGTCTCTACGGTGTGCTGGTCTCAC 825  
Db 260 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 280  
QY 826 CGGCCGCAAGATCATCATCTACTTACGAGAGTGGGTGCTCATGGTGGTGGTCTT 885  
Db 280 rGlyArgLysIleIleIleAspThrTyGlyGlyTrpGlyAlaHisGlyGlyGlyAlaPh 300  
QY 886 CTCGGGGAAGATCCCAACCAAGTTGATAGAGTGGTCTTACATTGTGAGACAGGCTGC 945  
Db 300 sSerGlyLysAspProThrLysValAspArgSerGlyAlaTyIleValArgGlnAlaI 320  
QY 946 TAAGAGCATTTGGCAAGTGCATAGCCAGAGGTGCATTGTGCAAGTGTCTTATGCCAT 1005  
Db 320 aLysSerIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyAlaI 340  
QY 1006 TGGTGTGCCGAGCTTTGTCTGTCTTTGTTGATGACACTATGGCACCAGGAGATCCATGA 1065  
Db 340 eGlyValProGluProLeuSerValPheValAspThrTyGlyThrGlyLysIleHis 360  
QY 1066 TAAGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTCAGCCCGGTATGATCTCCAT 1125  
Db 360 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerI 380  
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACA 1185

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Db 380 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyGlyHi 400
QY 1186 CTTGGCAGAGAGACCCCTGACTTCAATGGAAGTGGTCAAGCCCTCAAGTGGAGAA 1245
Db 400 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluLy 420
QY 1246 GGCC 1249
Db 420 sAla 421
|||
RESULT 6
US-10-425-114-51415
; Sequence 51415, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51415
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700748001_FLI.pep
US-10-425-114-51415
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Alignment Scores:
Pred. No.: 7,29e-193 Length: 422
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-51415 (1-422)
QY 4 CAAGCCCCACTCAACACACACCACT-----CTCTGCTCTTCT 45
Db 2 GlnAlaProLeuAsnHisThrSerProArgSerArgTyProPhe-LeuLeuPhePh 21
QY 46 CTACCTTTCAAGTTTAAAGTATTAAAGATGGCAGAGACATTCCTATTACCTCAGATC 105
Db 21 eTyLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 41
QY 106 AGTGACAGGAGACACCCCTGACAAGCTCTGCACCAAAATCTCCGATGCTGCTCGAGCG 165
Db 41 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 61
QY 166 TTGCCTTGAACAGGACCCAGACAGCAAGGTTGCCTGCGAAACATGCACCAAGACCACTT 225
Db 61 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 81
QY 226 GGTGATGTCCTCGGAGAGATCACCAAGCCCAAGCTTGACTAGGAGAGATCGTGG 285
Db 81 uValMetValPheGlyGluThrThrLysAlaAsnValAspTyTrpGluLysIleValAr 101
QY 286 TGACACCTCAGGAACATCGGCTTCTCTCAACAGATGGGACTTGATGCTGACAACATG 345
Db 101 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnC 121
QY 346 CAAGGTCTTGTAAACATTGAGCAGCAGACCCCTGATATTGCCAGGGGTGTCACGGCCA 405
Db 121 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 141
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QY 406 CTTTACCAAAAGACCCGAGGAATCGGTGCTGGAGACCAGGTCACATGTTTGGCTATGC 465
Db 141 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyAl 161
QY 466 CACGAGCAAAACCCAGAAATTGATGCCATTGAGTCATGTCATGCTTTCGCAACTAAACTCGGTGC 525
Db 161 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 181
QY 526 TCGTCTCACGAGGTTCCAAAGAACCGGAACTGTCGCCATGGTTGGAGCGCTGATGGAAAAAC 585
Db 181 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 201
QY 586 CCAAGTGACTCTGTCAGTATTACATGACCAACGGTGCCTATGGTTCCAGTTCGTGTCCACAC 645
Db 201 rGlnValThrValGluTyTrpAsnAspAsnGlyAlaArgValProIleArgValHisTh 221
QY 646 TGTGCTTATCTCCACCCCAACATGATGAGACTGTGACCAACGACCAAAATTCGAGCTGACCT 705
Db 221 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 241
QY 706 CAAGGAGCATGTGATCAAGCCGCTGATCCCGAAGAGTACCTTGATGAGAAGACCATTTT 765
Db 241 uLysGluHisValIleLysProValIleProGluLysTrpLeuAspGluLysThrIlePh 261
QY 766 CCACCTTGAAACCCCTCTGGCGGTTTTGTCAATTGGAGGTCCTCACGGTGATGCTGCTCAC 825
Db 261 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 281
QY 826 CGGCGGCAAGATCATCATCGATCTTACGAGGATGGGGTCTCATGTGTGGTGTCTTT 885
Db 281 rGlyArgLysIleIleIleAspThrTyGlyGlyTrpGlyAlaHisGlyGlyAlaPh 301
QY 886 CTCCGGGAAGGATCCCAACAAAGTGTAGAGTGGTGTCTTACATTTGTGAGACAGGCTGC 945
Db 301 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyTrpIleValArgGlnAlaAl 321
QY 946 TAAGAGCATTTGTCGCAAGTGCAGTACGACAGAGGTCATTTGCAAGTCTTATGCCAT 1005
Db 321 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyAlaAl 341
QY 1006 TGGTGTGCGCCGAGCCTTTGCTCTGCTTTTGTGACACCTATGGCACCGGGAAGATCCATGA 1065
Db 341 eGlyValProGluProLeuSerValPheValAspThrTyGlyThrGlyLysIleHisAs 361
QY 1066 TAAGAGATTTCTCAACATTTGTAAGGAGAACTTTGATTTTCAGGCCCGGTATGATCTCAT 1125
Db 361 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 381
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTTGAAGACTGCTGCATATGGACA 1185
Db 381 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyGlyHi 401
QY 1186 CTTCGGCAGAGAGACCCCTGACTTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGAGAA 1245
Db 401 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 421
QY 1246 GGCC 1249
Db 421 sAla 422
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## RESULT 7

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US-10-425-114-43754
; Sequence 43754, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 43754  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700654923\_FLI.pep  
US-10-425-114-43754

Alignment Scores:  
Pred. No.: 7.3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1  
US-10-734-698A-38 (1-1485) x US-10-425-114-43754 (1-423)

QY 4 CAGCCCTGCTGACACACACACT-----CTCTCTGCTCTCTT 45  
DB 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22  
QY 46 CTACCTTTCAAGTTTAAAGTATTAAAGATGGCAGAGACATCTCTATTACCTCAGAGTC 105  
DB 22 eTyrLeuSerSerPheLeuSerLeuMetAlaGluThrPheLeuPheThrSerGluSe 42  
QY 106 AGTGAACGAGGACACCCCTGACAACTCTCGACCAAAATCTCCGATGCTCTCGACGC 165  
DB 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62  
QY 166 TTGCTTGAACAGGACCCAGACAGAGAGTGGTCTCGGAAACATGACCAAGACCAACTT 225  
DB 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82  
QY 226 GGTCTATGCTCTCGGAGAGATCACCAAGGCCAGCTTACTACGAGAAATCGTGGC 285  
DB 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102  
QY 286 TGACACTGTCAGAAACATCGCTCTCTCAACAGATGCGGACTTGATGCTGACAACTG 345  
DB 102 gaepThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122  
QY 346 CAAGGTCTTGTAAACATTGAGCAGCAGCCTGATATTGCCAGGGTGTGCACGGCCA 405  
DB 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142  
QY 406 CCTTACCAAAAGACCCGAGAAATCGTCTGGAGACCAAGGTCACATGTTTGGCTATGC 465  
DB 142 sleuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162  
QY 466 CAGGACGAAACCCCAAGAAATGATGCTCATGATGCTGCTGCAACTAAATCGGTGC 525  
DB 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182  
QY 526 TGTCTTCACGAGGTTCGAAAGAACCTGCCCATGTTGAGCCCTGATGGGAAAC 585  
DB 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202  
QY 586 CCAAGTGACTGTGAGTATTACATGACCAAGCTGCATGCTTCCAGTTCGTGTCACAC 645  
DB 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaAa-gValProIleArgValHisTh 222  
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCGACGTGACCT 705  
DB 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242  
QY 706 CAAGGAGCATGTGATCAAGCCGCTGATCCCGGAGAAAGTACCTTGATGAGAACCACTTTT 765

DB 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
QY 766 CCACCTTGAAACCCCTCTGGCCGCTTTTGTTCATTTGGAGAGTCTCAGCGTGATGCTGCTCAC 825  
DB 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
QY 826 CGGCCGCAAGATCATCATCATCTTACCGAGAGATGGGTGCTCATGGTGGTGGTCTTT 895  
DB 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyGlyAlaPh 302  
QY 886 CTCGCCGGAAGATCCCAACAGGTTGATAGGAGTGGTCTTACATTTGTCAGACAGGCTGC 945  
DB 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaIleValArgGlnAlaAl 322  
QY 946 TAAAGACATTGTGCAAGTGGACTAGCCAGAAAGTGCATTGTGCAAGTCTCTTATGCCAT 1005  
DB 322 aLysSerIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyrAlaAl 342  
QY 1006 TGGTGTGCCGAGCCTTTGCTGCTTGTTCACACCTATGACCGGAGAACATCCATGA 1065  
DB 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362  
QY 1066 TAAAGACATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGGCCGGTATGATCTCCAT 1125  
DB 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382  
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGGACA 1185  
DB 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402  
QY 1186 CTTCCGCGCAGAGAGGACCTCTGACTTACATGGGAAGTGTCAAGCCCTCAAGTGGGAGAA 1245  
DB 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluL 422  
QY 1246 GSCC 1249  
DB 422 sAla 423

## RESULT 8

US-10-425-114-44216  
; Sequence 44216, Application US/10425114  
; Publication NO. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 44216  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700901925\_FLI.pep  
US-10-425-114-44216

Alignment Scores:  
Pred. No.: 7.3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-44216 (1-423)

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QY 4 CAAGCCCACTCAACACCAACCACCT-----CTCTCTGCTCTCTT 45
Db 3 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTTCAAGTTTAAAGATTAAAGATGCGAGAGACATTCTTATTATTCCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLeysSerIleLeysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCCCTGACAAGCTCTGCAACCAATCTCCGATCGCTGCTCGAGCC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACAGCAAGGTTGCTGCGAAACATGCAACAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCAATGCTTCGGAGAGATCACCAACGAGCCAACTGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCAGGAACATCGGCTTCGCTCAACAGATGCGAGCTTGATCGTGAACAATG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
QY 346 CAAGGTCTCTTAAACATTGAGCAGCAGAGCCCTGATATTGCCAGGGTGTGCACGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAAAGACCCGAGAAATCGTCTCGAGACCAAGGTCACTATGTTGGTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CAGGACGAAACCCCAAGATTGATGCCATTGATGATCTTCTGCAACTAAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TGTCTCACCGAGGTTCCGAAGAACCTGCTCCCATGTTGAGCCCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProThrLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGAATGTTAGTATTACAATGACAAACGGTGCCATGGTTCCAGTTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTATCTCCACCAATGATGATGAGCTGTGACCAACGAGAAATGCGAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAAGGACATGTGATCAAGCCGTTGATCCCGAGAGAGTACCTTGATGAGAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACCTTGAACCCCTTGGCCGTTTGTCTATTCGAGGTCCTCAGGTGATGCTGGTCTCAC 825
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCGACATCATCATCATCTACCGAGATGGGTGCTCATGGTGGTGGCTTT 885
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302
QY 886 CTCGGGAAGGATCCCAACCAAGTTGATAGGATGGTGTCTACATTTGTGAGACAGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
QY 946 TAAGACATTTGGCAAGTGGACTAGCCAGAAAGGTGCAATGTCGAAGTGTCTTATGCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaI 342
QY 1006 TGGTGTCCCGACCTTCTCTCTTGTTCACACCTATGCGACCGGAGACATCATCA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGGAGATTCTCAACATTTGTGAAGGAGAACTTTGATTTTCAGGCCCGGTATGATCTCCAT 1125
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Db 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY 1126 CAACCTTGATCTCAAGAGGGGTGGAAATAACAGAGTTCTTGAAGACTGCTGCATATGGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTGGCAGACAGAGACCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGACAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluLys 422
QY 1246 GGCC 1249
Db 422 sAla 423
RESULT 9
US-10-425-114-45712
; Sequence 45712, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45712
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700891875_FLI.pep
US-10-425-114-45712
Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1
US-10-734-698A-38 (1-1485) x US-10-425-114-45712 (1-423)
QY 4 CAAGCCCACTCAACACCAACCACCT-----CTCTCTGCTCTCTT 45
Db 3 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTTCAAGTTTAAAGATTAAAGATGCGAGAGACATTCTTATTATTCCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCCCTGACAAGCTCTGCAACCAATCTCCGATCGCTGCTCGAGCC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACAGCAAGGTTGCTGCGAAACATGCAACAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCAATGCTTCGGAGAGATCACCAACGAGCCAACTGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCAGGAACATCGGCTTCGCTCAACAGATGCGAGCTTGATCGTGAACAATG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
```

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QY 346 CAAGGTCCTTGTAAACATTGAGCAGCAGACCCCTGTATTTGCCAGGGTGTGCACGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAGAACCCGAGGAATCGGTGCTGAGACCCAGGGTCACATGTTGGCTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGACGAAACCCAGAAATGTATGTCATTCAGTTCATGTTCTTCCAACTAAACTCCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCGTCTCACAGAGTTCGCAAGAACCGAACCCTGCCATGTTGAGCGCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACATGACACCGTGCATGTTCCAGTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTCAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisaspGluThrValThrAsnAspGluIleAlaAspLe 242
QY 706 CAAGGAGCATGTGATCAAGCCGTGATCCGGAGAAGTACCTTGTGATGAGAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACTTGAACCCCTCGCGCTTTGCTCATTTGAGGTCTCAGCGTATGCTGGTCTCAC 825
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuth 282
QY 826 CGGCCCCAAGATCATCATCTACTTACGAGATGGGTGCTCATGGTGGTGGTCTTT 885
Db 282 rGlyArgLysIleIleIleaspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302
QY 886 CTCGGGAAGGATCCCAAGGTTGATAGGAGTGTGCTTACATTTGTGAGACAGGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
QY 946 TAAGACATGTGGCAAGTGGATAGCAGAGAGTGCATGTCAGTGTCTTATGCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyrAlaAl 342
QY 1006 TGTGTGCCGAGCCTTTGCTGCTTGTGACACCTATGACACCGGGAAGATCCATGA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGGAGATTCTCAACATTTGTAAGGAGAACTTTGATTTTCAGGCCCGGTATGATCTCCAT 1125
Db 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATACAGGTTCTTGAGACGTGCTGCATATGGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTCCGACAGAGGACCCCTGACTTTCATGCGGAAGTGTCAAGCCCTCAAGTGGAGAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
QY 1246 GGCC 1249
Db 422 sAla 423
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RESULT 10

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US-10-425-114-45723
; Sequence 45723, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 45723
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700896016_FLI.pep
US-10-425-114-45723
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Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1
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US-10-734-698A-38 (1-1485) x US-10-425-114-45723 (1-423)

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QY 4 CAAGCCCACTCAACACCACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 45
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPheLeuLeuPhePh 22
QY 46 CTACCTTCAAGTTTTTAAAGATTAAAGATGGCAGAGACATTCCTATTTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCTGCAAGCTCTGCAACCAATCTCCGATCTGCTGCTGACCG 165
Db 42 rValAsnGluGlyHisProAspLysLeuLysCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTCTGAACAGGACCCAGCAGCAGCAAGTTCCTCGCAACATGCACCAAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTATGTTCTTCGAGAGATCACCACCAAGGCCAACGTTGACTAGCAGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTGCGAGGAACATCGGCTTCGTCTCAAAACGATGTGGGACTTGATGCTGACACTG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
QY 346 CAAGGTCTCTGTAAACATTGAGCAGCAGACCCCTCATATTGCCAGGGTGTGCACGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAAAGACCCGAGGAAATCGGTGCTGAGACACCGGCTCATGTTTGGGTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGACGAAACCCAGAAATTTGATGCCATTTGAGTTCATGTTCTTGTGCAACTTAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCGTCTCACAGGTTTCGCAAGAACCGAACCCTGCCATGTTGAGCGCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACATGACACCGTGCATGTTCCAGTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTCAGCTGACCT 705
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Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242  
Qy 706 CAAGAGCATGTGATCAACCCGGTGATCCCGAGAGTACCTTGATGAGAACCATTTT 765  
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
Qy 766 CCACTTGAACCCCTCGGCCGTTTGTTCATTCGAGGTCTCACGGTGATGCTGGTCTCAC 825  
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
Qy 826 CGGCGCAAGATCATCATCATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTT 885  
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302  
Qy 886 CTCCGGGAAGGATCCACCAAGTTGATAGGAGTGGTGTTCATCTGAGACAGGCTGC 945  
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322  
Qy 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAAGGTGCATTGTGCAAGTGTCTTATGCCAT 1005  
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaAl 342  
Qy 1006 TGGTGTGCCGAGCCCTTGTCTGTCTTTGTTGACACCTATGGCACCGGGAAGATCCATGA 1065  
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362  
Qy 1066 TAAGGAGATCTCAACATTTGTAAGGAGAACTTTGATTTCAGGCCCGGTATGATCTCCAT 1125  
Db 362 pLysGluIleLeuAsnIleValLysGluAsnPheArgPheArgProGlyMetIleSerIl 382  
Qy 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGGACA 1185  
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402  
Qy 1186 CTTCGCGAGAGGAGCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245  
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluLys 422  
Qy 1246 GGCC 1249  
Db 422 sAla 423

## RESULT 11

US-10-425-114-51430  
; Sequence 51430, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 51430  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700901534\_FLI.pep  
US-10-425-114-51430

## Alignment Scores:

Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7

DB: 15 Gaps: 1  
US-10-734-698A-38 (1-1485) x US-10-425-114-51430 (1-423)  
Qy 4 CAAGCCCCACTCAACCCACCACCAACACT-----CTCTCTGCTCTTCTT 45  
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22  
Qy 46 CTACTCTTCAAGTATTTAAAGTATTAGATGGCAGAGACATTCTCTATTACTCAGAGTC 105  
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42  
Qy 106 AGTCAACGAGGACACCCCTGACAAAGCTCTGGACCAAAATCTCCGATGCTGCTCCGACGC 165  
Db 42 rValAsnGluGlyHisProAspLysLeuLysAspGlnIleSerAspAlaValLeuAspAl 62  
Qy 166 TTGCTCTTGAACAGGACCCAGACAGCAAGTTGCTTGGGAAACATGCACCAAGACCAACTT 225  
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82  
Qy 226 GGTCAATGCTCTCGAGAGATCACCAAGCCCAAGCTTCACTACGAGAGATCGTGG 285  
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102  
Qy 286 TGACACCTGACAGGAACATCGGCTTCTCTCAACGATGTGGGACTTGATGCTGACAACTG 345  
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122  
Qy 346 CAAGGCTCTTAAACATTTGAGCAGCAGACCCCTGTATATTCGCCAGGGTGTGACGGCCA 405  
Db 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142  
Qy 406 CTTTACCAAAAGACCCGAGGAATCGGTCTGTGGAGACCCAGGTGCATGTTTGGCTATGC 465  
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162  
Qy 466 CACGACGAAACCCAGAAATGTAGTCCATTCAGTTCATGTTCTTCAACTAACTCCGGTGC 525  
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182  
Qy 526 TCGTCTCACCGAGTTTCGCAAGAACCTGCCCATCTGCTGAGGCTGTATGGGAAAC 585  
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202  
Qy 586 CCAAGTGACTTTCAGTATTACATGACCAAGGTGCCATGTTCCAGTTCGTCTCCACAC 645  
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222  
Qy 646 TGTCTTATCTCCACCCCAACATGATGAGCTGTGACCAACGACGAAATTCAGAGCTGACCT 705  
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242  
Qy 706 CAAGGACATGTGATCAAGCCGGTATCCCGAGAGTACCTTGTATGAGAGACCACTTTT 765  
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
Qy 766 CCACCTGACCCCTCGCCGTTTGTTCATTTGGAGGTCTCTCACGGTGTATGCTGCTCAC 825  
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
Qy 826 CGGCGCAAGATCATCATCATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTT 885  
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302  
Qy 886 CTCCGGGAAGGATCCCAAGGTTGATGAGGTGGTCTTACATTTGTGAGACAGGCTGC 945  
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322  
Qy 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAGGTGCATTGTGCAAGTGTCTTATGCCAT 1005  
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaAl 342  
Qy 1006 TGGTGTGCCGAGCCCTTGTCTGTCTTTGTTGACACCTATGGCACCGGGAAGATCCATGA 1065

```

Db      342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY      1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGCCCGGATGATCTCCCAT 1125
Db      362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY      1126 CAACCTTGATCTCAAGGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGGACA 1185
Db      382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY      1186 CTTCCGAGAGAGACCCCTGACCTTCATCGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db      402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
QY      1246 GGCC 1249
Db      422 sAla 423

RESULT 12
US-10-425-114-53367
; Sequence 53367, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53367
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700901573_FLI.pep
US-10-425-114-53367

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Alignment Scores:
Pred. No.:      7,3e-193      Length:      423
Score:          2149.00      Matches:    409
Percent Similarity: 97.63%      Conservative: 3
Best Local Similarity: 96.92%      Mismatches: 3
Query Match:      78.20%      Indels:    7
DB:              15          Gaps:      1

US-10-734-698A-38 (1-1485) x US-10-425-114-53367 (1-423)

QY      4  CAAGCCCACTCAACACACACCACT-----CTCTCTCTCTCTCT 45
Db      3  GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY      46  CTACCTTCAAGTTTAAAGATTAAAGATGCGAGACATTCCTATTATTCCTCAGATC 105
Db      22  eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGlus 42
QY      106  AGTGAACAGGAGACACCTCGACAACTCTCGACCAAAATCTCCGATGCTGCTCGACGC 165
Db      42  rValanGluGlyHisProAspLysLeuLysAspGlnIleSerAspAlaValLeuAspAl 62
QY      166  TTGCTTGAACAGGCCAGACAGAGAGGTTGCTCGGAAACATGCACCAAGCAACTT 225
Db      62  aCysLeuGluGlnAspProAspSerLysValaCysGluThrCysThrLysThrAsnLe 82
QY      226  GGTGATGTTCTCGGAGATCACCACCAAGGCCAAGCTTGACTACGAGAAATCGTGG 285
Db      82  uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleVala 102

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## RESULT 13

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US-10-425-114-68219
; Sequence 68219, Application US/10425114
; Publication No. US20040034888A1

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QY      286  TCACACCTGCAGGAACATCGGCTTCGTCTCAAAACGATGGGACTTGATGCTGCAACTG 345
Db      102  gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
QY      346  CAAGTCCTTGTAAACATTGACGACGAGCCCTGATATTGCCAGGGTGTCCACGGCCA 405
Db      122  sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY      406  CTTTACCAAAAGACCCGAGAAATCGGTCTCGAGACCAAGGCTCACATGTTGGCTATGC 465
Db      142  sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY      466  CACGACGAAACCCAGAAATTGATGCCATTGATGATGATGCTTCTTGCACAACTCAAGTGC 525
Db      162  aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY      526  TCGTCTCACCGAGGTTCCGAAAGACCGACCTGCCCATGGTTGAGGCCCTGATGGGAAAC 585
Db      182  aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY      586  CCAAGTGACTGTTGAGTATTACAATGACAAACCGTGCCATGGTTCCAGTTTCGTGTCCACAC 645
Db      202  rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY      646  TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCAGCTGACCT 705
Db      222  rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242
QY      706  CAAGGAGACTGTGATCAAGCCGCTCATCCCGAGAGAGTACCTTGTGATGAGAACCACTTT 765
Db      242  uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY      766  CCACCTTGAAACCCCTCTGGCCGTTTTGTTCATTGAGAGTCTCACGGTGTGCTGCTCAC 825
Db      262  eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY      826  CGGCCCAAGATCATCATCTACGATCTTACCGAGGATGGGCTGCTCATGTTGGTGGTCTTT 885
Db      282  rGlyArgLysIleIleIleAspThrTyrGlyTyrGlyAlaHisGlyGlyGlyAlaPh 302
QY      886  CTCGGGGAAGNATCCACCAAGGTTGATAGAGTGTGCTTACATGTTGAGACAGGCTGC 945
Db      302  eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
QY      946  TAAGAGCATTGTGCAAGTGAAGTAGCCAGAGGTCATTGTGCAAGTGTCTTATGCCAT 1005
Db      322  aLysSerIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyrAlaAl 342
QY      1006  TGGTGTGCCCGAGCCCTTTGCTGCTTTTGTGACACCTATGSCACCCGGGAAGATCCATGA 1065
Db      342  eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY      1066  TAAGAGATTTCTCAACATTGTGAAGGAACTTTGATTTACGCCCGGCTGATGATCTCCAT 1125
Db      362  pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY      1126  CAACCTTCATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGGACA 1185
Db      382  eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY      1186  CTTCCGAGAGAGGACCCCTGACTTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db      402  sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
QY      1246  GGCC 1249
Db      422  sAla 423

```



```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68219
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700757167_FLI.pbp
US-10-425-114-68219

Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-68219 (1-423)

QY 4 CAAGCCCACTCAACCCACACACCACT-----CTCTGCTCTTT 45
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTATTAAAGATTAAGATGACAGACATCTTATTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCTGACAAGCTCTGCACCAATCTCCGATGCTGCTCGAGC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnLysSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACAGAGTTCCTCGCAACATGCACCAAGACCACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTAGTCTTCGAGAGATCACCACCAAGGCCAAGTTGACTACGAGAAGATCGTGC 285
Db 82 uValMetValPheGlyGluLeuThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCAGGAACATCGGCTTCGTCTCAACAGATGGGACTTGATGCTGACAATG 345
Db 102 gaSPThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnC 122
QY 346 CAAGTCTCTTAACATTGACGACGAGCCCTGATATTGCCAGGGTGTCCAGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAAAGACCCGAGGAATCGGTCTGAGACACAGGCTCACATGTTGGGTATGC 465
Db 142 sleuthrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGGAAGAAACCCCAAGAAATGATGCAATGATGATGATGATGATGATGATGATG 525
Db 162 athrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TGTCTCACCGAGTTCCGAAGACCGACCTGCCATGTTGAGCCCTGATGCGGAAC 585
Db 182 aargLeuThrGluValArgLysAsnGlyThrCysProThrLeuArgProAspGlyLysTh 202
QY 586 CCAAGTACTGTTAGTATTACAAATGACACCGTGCATGTTCCAGTTCGTGTCACAC 645
Pred. No.: 7,3e-193 Length: 423
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Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlnYalaArgValProIleArgValHisTh 222
QY 646 TGTCTTATCTCCACCCAAACATGATGAGACTGTACCAACGACCAAGAAATTCAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAACGAGCATGTGATCAAGCCGGTGATCCCGAGAAAGTACCTTCATGATGAGAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACCTTCAACCCCTCTGCGCCGCTTTGTCATTCGAGGTCCTCACGGTGAATGCTGCTCAC 825
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCGCAAGATCATCATCTACTTACGGAGGATGGGTCTCATGTCGTGCTGCTTT 885
Db 282 rGlyArgLysIleIleAspThrTyrGlyGlyTyrPheGlyAlaHisGlyGlyGlyAlaPh 302
QY 886 CTCCGGGAAGGATCCCAACCAAGTTGATAGAGTGGTCTTACATTTGTGACACAGGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValAlaGlnAlaAl 322
QY 946 TAACGACATTCGCAAGTGGACTAGCCAGAGGTGATTCGCAAGTGTCTTATGCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaAl 342
QY 1006 TGGTGTCCCGAGGCTTGTCTCTTTGTTGACACCTATGCGACCGGAGAGATCCATGA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGCAGATTCCTCAACATTTGTAAGAGGAACTTTGATTTCAGGCCCGGTATGATCTCCAT 1125
Db 362 pLysGluLeuLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerAl 382
QY 1126 CAACCTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTCCGACAGAGACCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluL 422
QY 1246 GGCC 1249
Db 422 sAla 423

RESULT 14
US-10-425-114-71903
; Sequence 71903, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71903
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700746279_FLI.pbp
US-10-425-114-71903

Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
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Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservativity: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-71903 (1-423)

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QY 4 CAAGCCCCACTCAACACACACACT-----CTCTCTGCTCTTCTT 45
Db 3 GlnAlaProLeuAenHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTTAAAGTATTAAAGATGGCAGAGACATTCCTATTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCAGACGCTCTCGACCAAAATCTCCGATCGCTGCTCCGACGC 165
Db 42 rValAenGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTCTTGAACAGGACCCAGACAGAGTTGCTCGAAACATGCAACCAAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTATGCTTCCGAGAGATCAACCAAGGCCAACGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCGAGAAACATCGCTTCCTCAACAGATGTTGGAGCTTGATCTGACAACTG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnC 122
QY 346 CAAGGTCCTTTGTAACATTCAGCAGCAGACCCCTGATATTGCCAGGCTGTGCACGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACAAAGACCCGAGAAATCGGTGTGAGACCAAGGTCATCATGTTGGCTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CAGGACGAAACCCAGATTTGATGCTTTCATGATGATGCTTTCGCACTAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCGTCTCACGAGGTTTCGAAGAACGGAACCTGCCATGTTGAGCGCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProThrLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACAAATGACCAACCGTGCCATGGTTCAGTTCGTGCCACAC 645
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAAGCAGCAAAATTCAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAAGGACGATGTCATCAAGCCGCTGATCCGGAAGAAGTACCTTGATGAGAAGACCAATTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACTTGAACCCCTCTGGCGGTTTTGTCAATTGAGGCTCTCAGGTCGATGCTGGTCTCAC 825
Db 262 eHisLeuAenProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCCCAGATCATCATGATACCTTACGAGAGATGGGTGCTCATGGTGGTGGCTTT 885
Db 282 rGlyArgLysIleIleAspThrTyrGlyGlyTyrGlyAlaHisGlyGlyGlyAlaPh 302
QY 886 CTCGCGGAAGGATCCCAACCAAGTTGATAGGAGTGTGCTTACATTGTGAGACAGGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaI 322
QY 946 TAAGACATTTGTGGCAAGTGGACTAGCCAGAGGTCATTTGTGCAAGTGTCTTATGCCAT 1005
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Db 322 aLysSerIleValAlaSerGlyLeuAlaArgGlyCysIleValGlnValSerTyrAlaI 342
QY 1006 TGGTGTGCCCGAGCCTTCTGCTGCTTTTGACACCTATGGCAGCGGAAGATCCATGA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHis 362
QY 1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGCCCGGTATGATCTCCAT 1125
Db 362 pLysGluIleLeuAenIleValLysGluAenPheAspPheArgProGlyMetIleSerIl 382
QY 1126 CAACCTTGATCTCAAGAGGGTGGGATTAACAGGTTCTTGAAGACTGCTGCATATCGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTGCGCAGAGGAGCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCCAAGTGGGAGAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluL 422
QY 1246 GGCC 1249
Db 422 sAla 423
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RESULT 15

US-10-425-114-71916  
; Sequence 71916, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 71916  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700747550\_FLI.pap  
US-10-425-114-71916

Alignment Scores:

Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservativity: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-71916 (1-423)

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QY 4 CAAGCCCCACTCAACACACACACT-----CTCTCTGCTCTTCTT 45
Db 3 GlnAlaProLeuAenHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTTAAAGTATTAAAGATGGCAGAGACATTCCTATTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCAGACGCTCTCGACCAAAATCTCCGATGCTGCTCCGACGC 165
Db 42 rValAenGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTCTTGAACAGGACCCAGACGAGTTCCTCGGAAACATGCAACCAAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
```

Search completed: August 25, 2005, 17:35:57  
Job time : 249 secs

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QY 226 GGTCTGCTTTCGGAGAGATCACCAAGCCCAAGCTTGACTAGGAGAAGATCGTGG 285
Db      |||||||
QY 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
Db      |||||||
QY 286 TGACACCTGCAGGAACATCGGCTTCGTCTCAAAACGATGTGGACTTGATGCTGACAACTG 345
Db      |||||||
QY 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
Db      |||||||
QY 346 CAAAGTCTCTTAAACATTGAGCAGAGAGCCCTGATATTGCCAGGGTGTGCACGGCCA 405
Db      |||||||
QY 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
Db      |||||||
QY 406 CTTTACCAAAAGACCGAGGAATCGGTCTCGAGACAGGCTCACATGTTTGGCTATGC 465
Db      |||||||
QY 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
Db      |||||||
QY 466 CACGACGAAACCCAGAAATGATGCCATTGAGTCATGTTCTTGCAACTTAAACTCGGTGC 525
Db      |||||||
QY 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
Db      |||||||
QY 526 TGTCTTCACCGAGTTTCGAAAGACCGAACCTGCCCATGGTTGAGGCCTGATGGGAAAC 585
Db      |||||||
QY 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
Db      |||||||
QY 586 CCAAGTGACTGTTGAGTATTACAATCAACACGCTGCCATGTTCCAGTTCGTGTCCACAC 645
Db      |||||||
QY 202 rGlnValThrValGluTyrTyAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
Db      |||||||
QY 646 TGTGCTTATCTCCACCAACATGAGACTGTGACCAACGACGACGAAATTCAGCTGACCT 705
Db      |||||||
QY 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242
Db      |||||||
QY 706 CAAAGAGCATGTGATCAACCGGTGATCCCGAGAGTACCTTGATGAGAGAACCATTTT 765
Db      |||||||
QY 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
Db      |||||||
QY 766 CCACCTTGAAACCTCTCGGCCGTTTGTCTCATTGGAGTCTCCTCAGGTGATGCTGCTCAC 825
Db      |||||||
QY 262 eHisLeuAenProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuth 282
Db      |||||||
QY 826 CGGCCGCAAGATCATCATGACTTACGAGAGATGGGTGCTCATGTTGGTGGTCTTT 885
Db      |||||||
QY 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyValaPh 302
Db      |||||||
QY 886 CTCCGGGAAGGATCCCAAGCTTGATAGAGTGTGCTTACATTGTGAGACAGGCTGC 945
Db      |||||||
QY 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
Db      |||||||
QY 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAGAGTGCATTGTGCAAGTGTCTTATGCCAT 1005
Db      |||||||
QY 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaAl 342
Db      |||||||
QY 1006 TGTGTGCCCGAGCCTTCTGCTCTTCTGTTGACACCTATGGCACCGGGAAGATCCATGA 1065
Db      |||||||
QY 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
Db      |||||||
QY 1066 TAAGAGATTCTCAACATTGTGAAGAGAACTTTGATTTACGGCCCGGTATCATCTCCAT 1125
Db      |||||||
QY 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
Db      |||||||
QY 1126 CAACCTTGATCTCAAGAGGGTGGGNAATAACAGGTCTTGAAGACTGCTGCATATGGACA 1185
Db      |||||||
QY 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaIaIaTyrGlyHi 402
Db      |||||||
QY 1186 CTTCCGACAGAGGACCCCTGACTTCATGTTGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db      |||||||
QY 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluL 422
Db      |||||||
QY 1246 GGCC 1249
Db      |||
QY 422 sAla 423
Db      |||
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 17:03:11 ; Search time 60 Seconds  
(without alignments)  
4762.730 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 2748  
Sequence: 1 ACCCAAGCCCCCTCAACCA.....CAAAGAATGTTCAGATT 1485

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cn2\_1/USPTO\_spool\_p/US10734698/runat\_25082005\_105401\_10285/app\_query.fasta\_1.1671  
-DB=PIR -QPMT=fastan -SUPTX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -LIST=45  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10734698 @CN 1 1.80 @runat\_25082005\_105401\_10285 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1985	72.2	393	2	S46538 methionine adenosy
2	1983	72.2	393	2	S38875 methionine adenosy
3	1947	70.9	393	2	JQ0410 methionine adenosy
4	1940	70.6	393	2	C86155 S-adenosylmethioni
5	1937	70.5	393	2	JN0131 methionine adenosy
6	1932.5	70.3	396	2	T10710 methionine adenosy
7	1920.5	69.9	397	2	S68352 methionine adenosy
8	1900.5	69.2	394	2	T06180 methionine adenosy
9	1884	68.6	390	2	S46540 methionine adenosy
10	1872	68.1	390	2	G84785 probable s-adenosy
11	1857	67.6	390	2	S49491 methionine adenosy
12	1803	65.6	366	2	S66351 methionine adenosy
13	1742	63.4	360	2	T06592 methionine adenosy
14	1316.5	47.9	395	1	S27257 methionine adenosy

15	1310.5	47.7	395	2	A37118 methionine adenosy
16	1274.5	46.4	382	2	T39451 methionine adenosy
17	1268.5	46.2	396	2	A47151 methionine adenosy
18	1268	46.1	397	2	S06114 methionine adenosy
19	1264	46.0	395	2	S65800 methionine adenosy
20	1262.5	45.9	395	1	S27363 methionine adenosy
21	1209.5	44.0	404	2	T34085 hypothetical prote
22	1209.5	44.0	404	2	T34084 hypothetical prote
23	1205	43.9	419	2	T16856 hypothetical prote
24	1198.5	43.6	382	2	S51425 methionine adenosy
25	1198	43.6	403	2	T20070 hypothetical prote
26	1191.5	43.4	384	2	A31398 methionine adenosy
27	1180	42.9	359	2	T47208 methionine adenosy
28	1167.5	42.5	399	2	D84062 S-adenosylmethioni
29	1156.5	42.1	405	2	S41917 methionine adenosy
30	1137	41.4	395	2	G72228 S-adenosylmethioni
31	1114	40.5	400	2	D69657 methionine adenosy
32	1106.5	40.3	391	2	D97251 S-adenosylmethioni
33	1104	40.2	399	2	AD1654 S-methionine adeno
34	1100.5	40.0	389	2	D81042 S-adenosylmethioni
35	1096.5	39.9	398	2	F89964 probable methionin
36	1093.5	39.8	389	2	E81986 S-methionine adeno
37	1091	39.7	399	2	AH1282 S-methionine adeno
38	1072	39.0	363	2	T26385 hypothetical prote
39	1069.5	38.9	384	2	AB0877 S-adenosylmethioni
40	1068.5	38.9	384	1	SYECSM methionine adenosy
41	1068.5	38.9	384	2	B91106 methionine adenosy
42	1068.5	38.9	384	2	E85951 methionine adenosy
43	1062.5	38.7	396	2	G97955 methionine adenosy
44	1060	38.6	385	2	E82319 S-adenosylmethioni
45	1058	38.5	388	2	S51671 methionine adenosy

ALIGNMENTS

RESULT 1

S46538  
methionine adenosyltransferase (EC 2.5.1.6) - tomato  
N/Alternate names: S-adenosyl-L-methionine synthetase  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S46538; S38874  
R/Submitter: J. Pintor-Toro, J.A.; Pardo, J.M.  
A/Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res.  
Plant Mol. Biol. 25, 217-227, 1994  
A/Reference number: S46538; MUID:94289646; PMID:8018871  
A/Accession: S46538  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-393 <ESP>  
A/Cross-references: UNIPROT:P43280; EMBL:Z24741; NID:G429103; PIDN:CAA80865.1; PID:G4291  
C/Superfamily: methionine adenosyltransferase  
C/Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 8.54e-151 Length: 393  
Score: 1985.00 Matches: 374  
Percent Similarity: 97.69% Conservative: 6  
Best Local Similarity: 96.14% Mismatches: 9  
Query Match: 72.23% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S46538 (1-393)

QY	80	GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTTGACAGCTCTGCAC	139
DB	2	GlutThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspLysLeuCysAsp	21
QY	140	CAATCTCCGATGCTGCTCGACCTTGCCTTGAACAGGACCCAGACAGCAGGAGTTGCC	199
DB	22	GlnIleSerAspAlaValLeuAspAlaCysLeuGluInAspProGluSerIysValAla	41
QY	200	TGCGAAACATGCACCAAGACCAACTTGTGTCATGTTTCGGAGAGATCACCACCAAGGCC	259

|||||  
42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
260 AACGTTGACTACGAGAAGATCGTGGTGTACACCTGCAGGAAACATCGGCTGCTCTCAAAC 319  
Db |||||  
62 lIeValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsp 81  
Qy |||||  
320 GATGTGGGACTTGCTGCACAACTGCAGAGTCCCTGTAAACATTTGAGCAGCAGACCGCT 379  
Db |||||  
82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnGlnSerPro 101  
Qy |||||  
380 GATATTGCCACGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTCTCGA 439  
Db |||||  
102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
Qy |||||  
440 GACACGGGTGCATGTTTGGCTATGCCACGACGAGACCCCAAGAAATTCATGATGATGAGT 499  
Db |||||  
122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
Qy |||||  
500 CATGTTCTTGAACAACTCGTCTCCTCACGGAGTTCGCAAGACCGGACCTGCG 559  
Db |||||  
142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy |||||  
560 CCATGTTGAGGCTGATCGGAAAAACCCAAAGTGAAGTGTGATTAACAATGACACCGT 619  
Db |||||  
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Qy |||||  
620 GCATGTTCCAGTTCGTGTCACACTGTCCTTCTCACCACCAACATGATGAGACTGTG 679  
Db |||||  
182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy |||||  
680 ACCACGACGAATTCGACCTGACCTCAAGGACATGTGATCAAGCCGTGATCCCGAG 739  
Db |||||  
202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy |||||  
740 AAGTACTTGTAGAGAAGACCAATTTTCCACTTGAACCCCTCTCGGCCGTTTGTCTATTGGA 799  
Db |||||  
222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
Qy |||||  
800 GTCTCTACGGTGATGCTGGTCTCACCGGCCGCAAGATCATCATGACTTACCGAGGA 859  
Db |||||  
242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
Qy |||||  
860 TCGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACAGGTTGATAGGAGT 919  
Db |||||  
262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
Qy |||||  
920 GGTGTTTACATTGTGAGACAGGCTGCTAAGACATTTGTGGCAAGTGGACTAGCCAGAAGG 979  
Db |||||  
282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgArg 301  
Qy |||||  
980 TGCATTGTCAAGTGTCTTATGCCATTGTGTGTCGGAGCCCTTGTCTGCTTTGTTGAC 1039  
Db |||||  
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Qy |||||  
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322 ThrTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341  
Qy |||||  
1100 GATTTCCAGCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db |||||  
342 AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLysArgGlyGlyAsnArgArg 361  
Qy |||||  
1160 TTCTTGAAGACTGCTGCATATGACATTCGTCGAGAGGACCTTCGACTTCAATGAGGAA 1219  
Db |||||  
362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
Qy |||||  
1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db |||||  
382 ValValLysProLeuLysTrpGluLys 390

methionine adenosyltransferase (EC 2.5.1.6) - tomato  
N:Alternate names: S-adenosyl-L-methionine synthetase  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S46539; S38875  
R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.  
Plant Mol. Biol. 25, 217-227, 1994  
A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res  
A:Reference number: S46538; MUID:94289646; PMID:8018871  
A:Accession: S46539  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-393 <ES2>  
A:Cross-references: UNIPROT:P43281; EMBL:224742; NID:9429105; PIDN:CAA80866.1; PID:942911  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase  
  
Alignment Scores:  
Pred. No.: 1,24e-150 Length: 393  
Score: 1983.00 Matches: 371  
Percent Similarity: 97.69% Conservative: 9  
Best Local Similarity: 95.37% Mismatches: 9  
Query Match: 72.16% Indels: 0  
DB: 2 Gaps: 0  
US-10-734-698A-38 (1-1485) x S38875 (1-393)  
  
Qy 80 GAGCATTCTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTTGACAAAGCTCTGCGAC 139  
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2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
Qy 140 CAATCTCCGATGCTGCTCGAGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
Db |||||  
22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluSerLysValAla 41  
Qy 200 TCGAAAACATCCACCAAGACCAACTTGTCTATGCTTTCGAGAGAGATCACCACCAAGGCC 259  
Db |||||  
42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
Qy 260 AACGTTGACTACGAGAAGATCGTGGTGTACACCTGCAGGAAACATCGGCTTGTCTCAAC 319  
Db |||||  
62 AsnIleAspTyrGluLysIleValArgAspThrCysArgGluIleGlyPheValSerPro 81  
Qy 320 GATGTGGGACTTGCTGCACAACTGCAGAGTCCCTGTAAACATTTGAGCAGCAGACCGCT 379  
Db |||||  
82 AspValGlyLeuAspAlaAspAsnCysArgValLeuValAsnIleGluGlnGlnSerPro 101  
Qy 380 GATATTGCCACGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTCTCGA 439  
Db |||||  
102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
Qy 440 GACACGGGTGCATGTTTGGCTATGCCACGACGAGACCCCAAGAAATTCATGATGATGAGT 499  
Db |||||  
122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
Qy 500 CATGTTCTTGAACAACTCGTCTCCTCACGGAGTTCGCAAGACCGGACCTGCG 559  
Db |||||  
142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy 560 CCATGTTGAGGCTGATCGGAAAAACCCAAAGTGAAGTGTGATTAACAATGACACCGT 619  
Db |||||  
162 SerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrHisAsnAspGly 181  
Qy 620 GCATGTTCCAGTTCGTGTCACACTGTCCTTCTCACCACCAACATGATGAGACTGTG 679  
Db |||||  
182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy 680 ACCACGACGAATTCGACCTGACCTCAAGGACATGTGATCAAGCCGTGATCCCGAG 739  
Db |||||  
202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy 740 AAGTACTTGTAGAGAAGACCAATTTTCCACTTGAACCCCTCTCGGCCGTTTGTCTATTGGA 799  
Db |||||

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Db      222 LysTyrLeuAspGluAenThrIlePheHisLeuAenProSerGlyArgPheValIleGly 241
QY      800 GGTCTCAGCGTATGCTGCTCACCAGCGGCAAGATCATCATCATGATATTACGAGGA 859
Db      242 GlyProHisGlyAspIleGlyLeuThrGlyArgGlyIleIleAspThrThrGlyGly 261
QY      860 TGGGGTGCATGCTGGTGGTCTTCTCCGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY      920 GTGTCTTACATTGTGAGACAGCTGCTAGACATGTCGCAAGTGGAGTACCGAGAGG 979
Db      282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
QY      980 TGCAATGTGCAAGTGTCTTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
Db      302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY      1040 ACCTATGGCACCGGGAAGATCCATGATAAGGAGATCTCAACATTGTGAAGGAACTTT 1099
Db      322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341
QY      1100 GATTTCAGCCCGGTATGATCCATCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
Db      342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLeuArgGlyAsnGlyArg 361
QY      1160 TTCTTGAAGACTGCTCATATGACACTTCGCGAGAGGACCCCTGACTTCACATGGGAA 1219
Db      362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTrpGlu 381
QY      1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db      382 ValValLysProLeuLysTrpAspLys 390

RESULT 3
JQ0410
methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0410
R:Peleman, J.; Saito, K.; Cottyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D.
Gene 84, 359-369, 1989
A:Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene f
A:Reference number: JQ0410; MUID:90128280; PMID:2482229
A:Accession: JQ0410
A:Molecule type: DNA
A:Residues: 1-393 <PEL>
A:Cross-references: UNIPROT:P17562; GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C:Genetics:
A:Gene: sam-2
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. NO.:          9.46e-148      Length:          393
Score:             1947.00        Matches:         360
Percent Similarity: 96.92%        Conservative:     17
Best Local Similarity: 92.54%      Mismatches:      12
Query Match:       70.85%         Indels:           0
DB:                2              Gaps:            0

US-10-734-698A-38 (1-1485) x JQ0410 (1-393)

QY      80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACCCCTGACAGCTCTGGGAC 139
Db      2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY      140 CAAATCTCCGATGCTGCTCCTCCAGCGCTTCTTGAACAGGACCCAGACAGCAAGGTGCC 199
Db      22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGluAspProAspSerLysValAla 41
QY      200 TGCAGAAACATGCACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAGGCC 259
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RESULT 4  
C86155

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Db      62 ThrIleAspTyrGluLysIleValArgAspThrCysArgSerIleGlyPheIleSerAsp 81
QY      320 GATGGGACATTGATGCTGACAACTGCAAGGTCTTGTAAACATTGAGCAGCAGAGCCCT 379
Db      82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY      380 GATATTGCCAGGGTGTGCACGGCCACCTTACCAGAAACACCCAGAGAAATCGGTCTGGA 439
Db      102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluAspIleGlyAlaGly 121
QY      440 GACAGGGTGCATGCTTTGGCTATGCCACGACGAGAAACCCAGAGATTGATGCTATTGAGT 499
Db      122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
QY      500 CATGTTCTGCAACTAAACTCGGTGCTCTCACCAGAGTTTCGCAAGAACGAACTGTC 559
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QY      560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGAGATATTACATGACACCGT 619
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QY      620 GCCATGGTTTCAGTTCGTTCCACACTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db      182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY      680 ACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCGGAG 739
Db      202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProIleIleProGlu 221
QY      740 AAGTACCTTGATGAGAGAACCATTTTCCATTGAAACCCCTCTGGCCGTTTGTCTATTGGA 799
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QY      800 GGTCTCAGCGTATGCTGCTCTCACCGCGCAGAGATCATCATCATGATCTTACCGAGGA 859
Db      242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThrGlyGly 261
QY      860 TGGGGTGCATGCTGGTGGTCTTCTCCGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY      920 GGTGTTTACATTGTGAGACAGCTGCTAAGAGCATTTGGGCAAGTGGAGTACCGCAGAGG 979
Db      282 GlyAlaTyrIleValArgGlnAlaLysSerValValAlaAsnGlyMetAlaArg 301
QY      980 TGCATTGTGCAAGTGTCTTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
Db      302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY      1040 ACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099
Db      322 ThrTyrGlyThrGlyLeuIleProAspLysGluIleLeuLysIleValLysGluThrPhe 341
QY      1100 GATTTCCAGCCCGGTATGATCTCCATCAACCTTGTGATCTCAAGAGGGGTGGGAAATACAGG 1159
Db      342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361
QY      1160 TTCTTGAAGACTGCTCATATGACACTTCGCGAGAGGACCCCTGACTTCACATGGGAA 1219
Db      362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTrpGlu 381
QY      1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db      382 ValValLysProLeuLysTrpAspLys 390
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S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86155  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86155  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-393 <STO>  
A:Cross-references: UNIPROT:P23686; GB:AE005172; NID:g9972389; PIDN:AAG10639.1; GSPDB:GN  
C:Genetics:  
C:Map position: 1  
C:Superfamily: methionine adenosyltransferase

Alignment Scores:  
Pred. No.: 3,44e-147 Length: 393  
Score: 1940.00 Matches: 363  
Percent Similarity: 96.40% Conservative: 12  
Best Local Similarity: 93.32% Mismatches: 14  
Query Match: 70.60% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x C86155 (1-393)

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Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCGAGTGTCTCTCAGCTTCAGCTTGTACAGGACCCAGACGAGGTGCC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41  
QY 200 TCGCAACATGCACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCAACAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AACGTTGACTACGAGAAGATCGTGGTGACACCTCGAGAAACATCGGCTTCGTCAAC 319  
Db 62 ThrValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCTCTTGAACATTTGACGACGAGCCCT 379  
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QY 380 GATATTGCCAGGTTGTGCACGGCCACCTTACCAAAAGACCCGAGAAATCGTCTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysCysProGluGluIleGlyAlaGly 121  
QY 440 GACCAAGGTCACATGTTGGCTATGCCACGACGAAACCCCAAGATTGATGCAATGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTGCAACTTAACTCGGTCTGTCTCACCAGGTTGCGAAGAACCGACCTGCG 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CCATGTTGAGCGCTGATGGGAAACCCCAAGTACTGTTGAGTATTACAATCACACCGT 619  
Db 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAspLysGly 181  
QY 620 GCCATGTTCCAGTTCGTCGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201

QY 580 ACCAACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaAargAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGGCCGCTTTTGTTCATTTGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCTCAGCGTGATGCTGCTCTCACCGCCGCGAAGATCATCATCGATCTACTTCAGGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
QY 860 TGGGGTCTCATGCTGTGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGTAGTAGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGTGACAGCGCTGCTAAGACGATTTGTGGCAAGTGGACTAGCCAGAGG 979  
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QY 980 TGCATTTGTGAAGTGTCTTATGCCATTGCTGTGCCCGAGCCCTTGTCTGTCTTGTTCGAC 1039  
Db 302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGCGACCGGAGAGATCATGATAAGGAGATTCTCAACATTTGTGAAGGAGAACTTT 1099  
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QY 1100 GATTTCAAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyAsnGlyArg 361  
QY 1160 TTCTTGAAGACTGCTGATATGACATTCGCGAGAGAGGACCCCTGACTTCACATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

RESULT 5  
JN0131  
methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana  
N:Alternate names: S-adenosylmethionine synthetase  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: JN0131  
R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van N  
Plant Cell 1, 81-93, 1989  
A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop  
A:Reference number: JN0131; MUID:92386056; PMID:2535470  
A:Accession: JN0131  
A:Molecule type: DNA  
A:Residues: 1-393 <PEL>  
A:Cross-references: UNIPROT:P23686; GB:M55077; NID:g166871; PIDN:AAA32868.1; PID:g166872  
A:Experimental source: var. K85  
A:Note: the sequence derived from var. Columbia differs from that shown in having 117-G  
C:Comment: S-Adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio  
A:Gene: sam-1  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 5.99e-147 Length: 393  
Score: 1937.00 Matches: 362  
Percent Similarity: 96.40% Conservative: 13  
Best Local Similarity: 93.06% Mismatches: 14  
Query Match: 70.49% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x JN0131 (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTCAAGAGGAGCACCTCACAAGCTCTCGCAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAATCTCCGATCTGCTCTCGAGCGTTCCTTGAACAGGACCCAGACAGCAAGTTGCC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41  
QY 200 TGGAAACATGACCAAGACCACTTGGTTCATCGTCTCGAGAGATCAACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrLysAla 61  
QY 260 AACGTTGACTACGAGAGATCGTCGTGACACCTGCAGGAACATCGGCTCTCTCAAC 319  
Db 62 ThrValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
QY 320 GATGTGGACTTGATCTGCAACTGCAAGTCTTGTAAACATTTGAGCAGCAGACCTCT 379  
Db 82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnSerPro 101  
QY 380 GATATTGCCAGGCTGTGCAGCGCCACCTTACCAGAGACCCGAGGAAATCGGTCTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysCysProGluAspIleGlyAlaGly 121  
QY 440 GACAGGGTCACATGTTTGGCTATGCCACGAGCAAAACCCAGAAATTTGATGCTTGGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTGCAACTAACTCGGTGCTCTCACCAGGTTTCGCAAGACCGAACCTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CCATGTTGAGCGCTGATCGGAAACCCCAAGTACTGTTGAGTATTACATCAACAGCT 619  
Db 162 AlaIlePheArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspLysGly 181  
QY 620 GCATGTTCCAGTTCGTGTCTGCACACTGTGCTTATCTCCACCAACATGATGAGCTGTG 679  
Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCACGAGCAATTCGACTGACCTCAAGAGAGCTGATGATCAAGCGGTGATCCCGAG 739  
Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AGTACTTTCATGAGAGACCAATTTTCCACTTGAACCCCTCTGGCGGTTTGTCTATGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTTCACGGTGATGCTGTCTCACCGCGCGCAAGATCATCATGATACTTACCGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTGCTCATGTTGGTGGTCTTCTCCGGAAGGATCCCAAGGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGAGAGAGCTGCTAAGACATTTGGCAAGTGGACTACCGAAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaAsnGlyMetAlaArgArg 301  
QY 980 TGCATTGTGCAAGTGTCTTATGCTTGTGTCGCGGAGCCTTGTGTCTTGTGTGAC 1039  
Db 302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAAGAGATTTCTCAACATTTGTGAAGGAACTTT 1099  
Db 322 ThrTyrGluThrGlyLeuIleProAspLysGluIleLeuLysIleValLysGluSerPhe 341  
QY 1100 GATTTGAGCCCGGATGATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATACAGG 1159  
Db 342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyThr 361

QY 1160 TTCTTGAAGACTGCTGCATATCGACACTTCGCAGAGAGACCCCTGACTTCATCGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGGTCAGCCCTCAAGTGGGAGAAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

## RESULT 6

T10710

methionine adenosyltransferase (EC 2.5.1.6) - clove pink

N:Alternate names: S-adenosylmethionine synthetase

C:Species: Dianthus caryophyllus (clove pink)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

R:Larsen, P.B.; Woodson, W.R.

submitted to the EMBL Data Library, April 1991

A:Description: Cloning and nucleotide sequence of a s-adenosylmethionine synthetase cDN

A:Reference number: Z17091

A:Accession: T10710

A&gt;Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-396 &lt;LAR&gt;

A:Cross-references: UNIPROT:P24260; EMBL:M61882; NID:g167961; PID:g304637

C:Genetics:

A:Gene: SAM2

C:Function:

A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyro

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

## Alignment Scores:

Pred. No.:	1-38e-146	Length:	396
Score:	1932.50	Matches:	364
Percent Similarity:	95.90%	Conservative:	10
Best Local Similarity:	93.33%	Mismatches:	15
Query Match:	70.32%	Indels:	1
DB:	2	Gaps:	1

US-10-734-698A-38 (1-1485) x T10710 (1-396)

QY 77 GAGAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGGACACCTGACAAAGTCTGC 136  
Db 5 AlaAspThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 24  
QY 137 GACCAATCTCGATCTGCTCTCGACCTGCTTGAACAGGACCCAGACAGCAAGTTT 196  
Db 25 AspGlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaGluSerLysVal 44  
QY 197 GCCTGCGAAACATGCACCAAGACCAACTTGGTTCATGTCCTTCGGAGAGATCACCAAG 256  
Db 45 AlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLys 64  
QY 257 GCCAACGTTGACTACGAGAAGATCGTCGTGACACCTCGAGGAACATCGGCTTCGTCTCA 316  
Db 65 AlaAsnValAspTyrGluLysIleValAlaAspThrCysArgGluIleGlyPheValSer 84  
QY 317 AACGATGCGGACTGATCTGACACTGCAAGTCCTTGTAAACATTTGAGCAGCAGACG 376  
Db 85 ProAspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnSer 104  
QY 377 CCTGATATTCAGGCGGTGTCAGCGGCACCTTACAAAAGACCCGAGGAATCGGTGCT 436  
Db 105 ProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluAspIleGlyAla 124  
QY 437 GGAGACCAAGGTCACATGTTTGGCTTATGCCAGCGAGAAACCCCAAGAAATTTGATGCCATTG 496  
Db 125 GlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 144  
QY 497 AGTCATGTTCTTGCACTAAACTCGTCTGCTCACCAGAGGTTTCGCAAGACGGAACC 556  
Db 145 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 164

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QY 557 TGCCCATGTTGAGGCTCATGGGAAACCCCAAGTGACGTGTTGAGTATTACAAATGACAAC 616
Db 165 CysAlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnGluAsn 184
QY 617 GGTGCCATGGTTCAGTTCGTGTCCACACTGTGCTTATCTCCACCCAAACATGATGAGACT 676
Db 185 GlyAlaMetValProileargValHisThrValLeuIleSerThrGlnHisAspGluThr 204
QY 677 GTGACCAACGACGAATTCGAGTGCACCTCAAGGAGCAGTGTGATCAAGCCGGTGTATCCGG 736
Db 205 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 224
QY 737 GAGAGTACCTTCATGAGAAGACCAATTTCCACTTGAACCCCTCGGCCGTTTCTCATTT 796
Db 225 GluLysTrpLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 244
QY 797 GGAGGTCTCCAGCGTGATGCTGTCTCACCGCCGCAAGATCATCATCATATCTTACGGA 856
Db 245 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTrpGly 264
QY 857 GGATGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGTTGATAGG 916
Db 265 GlyTrpGlyAlaHisGlyGlyGlyAlaPheSerArgLysAspProThrLysValAspArg 284
QY 917 AGTGGTGCTTACATTTGTGAGACAGGCTGCTAAGAGCATTGTGCGAAGTGCAGTACGAGA 976
Db 285 SerGlyAlaTrpIleAlaArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 304
QY 977 AGGTGCTATTGTGCAAGTGTCTTATGCTATGCTGTGTGTCGCCGAGCCTTTGTCTCTTTGTT 1036
Db 305 ArgCysIleValGlnIleSerTrpAlaIleGlyValProGluProLeuSerValPheVal 324
QY 1037 GACACCTATGGACCCGGGAAGATCCATGATAGAGAGATTCTCAACATTTGTAAGGAGAAC 1096
Db 325 AspThrTyrGlyThrGlyLysIleHisAspArgGluIleLeuLysIleValLysGluAsn 344
QY 1097 TTTGATTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156
Db 345 PheAspPheArgProGlyMetIleAlaIleAlaLeuAspLeuLysGlyGlyGlyGlyGlyGly 363
QY 1157 AGGTCTCTGAAGACTGCTGCATATGACACTTCGCGAGAGAGACCCCTGACTTTCATGG 1216
Db 364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 383
QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db 384 GluAlaAlaLysThrLeuLysTrpGluLys 393

RESULT 7
S66352
methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66352; S52218
R:Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries
A:Reference number: S66351; MUID:96194463; PMID:8624412
A:Accession: S66352
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <OM>
A:Cross-references: UNIPROT:P49613; EMBL:X82077
R:Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, October 1994
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.
A:Reference number: S52218
A:Accession: S52218
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364, 'PEDSCIWTFW' <GOW>
A:Cross-references: EMBL:X82077; NID:g609224; PIDN:CAA57581.1; PID:g609225
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C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 1,26e-145 Length: 397  
Score: 1920.50 Matches: 362  
Percent Similarity: 96.89% Conservative: 12  
Best Local Similarity: 93.78% Mismatches: 11  
Query Match: 69.89% Indels: 1  
DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x S66352 (1-397)

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QY 80 GAGACATTCCTATTATTACCTCAGAGTCAGTGAACGAGGACACCTGTGACAAAGCTCTGCGAC 139
Db 4 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 23
QY 140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199
Db 24 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 43
QY 200 TCGGAACATGCACAGACCAACTTGGTCTATGCTCTTCGGAGAGATCACCACCAAGGCC 259
Db 44 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 63
QY 260 AACGTTGACTACGAGAGATCGTGTGACACCTGCAGGAACATCGGCTTCGTCTCAAC 319
Db 64 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsp 83
QY 320 GATGTGGACTTGATGTGACAACTGCAAGGTCTCTTTAAACATTTGAGCAGCAGAGCCCT 379
Db 84 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 103
QY 380 GATATGTCAGGCTGTGACGGCCACTTACCAAAAGACCCGAGGAAATCGGTCTCGGA 439
Db 104 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluAspIleGlyAlaGly 123
QY 440 GACCAGGTGCATGTTTGGCTATGCCACGACGAAACCCAGAAATTCGATGCCATTGAGT 499
Db 124 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 143
QY 500 CATGTTCTTCAACTAAACTCGGTCTGCTCTCACCGAGGTTTCGCAAGAACCGGCTGC 559
Db 144 HisValLeuAlaThrLysLeuGlyAlaSerLeuThrGluValArgLysAsnGlyThrCys 163
QY 560 CCATGTTGAGCCCTGATGGGAAAACCCCAAGTGAAGTGTGAGTATTACAAATGACACCGT 619
Db 164 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspLysGly 183
QY 620 GCCATGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 184 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 203
QY 680 ACCAACGACGAAATTCGACGTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAG 739
Db 204 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 223
QY 740 AAGTACCTTGATGAGAGACCATTTTCCATTGAACCCCTCTGGCCGCTTTTGTCAATGGA 799
Db 224 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheArgHisGly 243
QY 800 GGTCTCTACGCTGATGCTGTCTCACCGCGCGCAAGATCATCATCATGATCTTACCGAGA 859
Db 244 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTrpGlyGly 263
QY 860 TGGGGTGTCTATGGTGGTGGTCTTCTTCCGGGAAGGATCCCAAGGTTGATAGGAGT 919
Db 264 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 283
QY 920 GGTGCTTACATTTGAGACAGCCTGCTTAAGAGCATTGTGGCAAGTGGAGTACCCAGAGG 979
Db 284 GlyAlaTyrIleValArgGluAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 303
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QY 980 TGCAATGTCAGTGTCTTATGCAATGTTGGTGTCCCGAGCCTTTGTCTGTCTTTGTTGAC 1039  
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Db 304 CysLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 323  
|||:|||||  
QY 1040 ACCTATGGCACCGGAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099  
|||:|||||  
Db 324 SerTyrGlyThrGlyLysIleProAspArgGluIleLeuAsnIleValLysGluAlaPhe 343  
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QY 1100 GATTTCAGGCCCGGTATGATCTCCATCAACCTTTGATCTCAAGGGGTGGGAATAACAGG 1159  
|||:|||||  
Db 344 AspPheArgProGlyMetIleSerIleSerLeuAspLeuArgGlyGlyAsnGlyArg 363  
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QY 1160 TTC---TTGAAGACTGCTGATATGACACTTCGGCAGAGAGACCTGACTTCACATGG 1216  
|||:|||||  
Db 364 PheLeuLeuLysThrAlaAlaTyrGlyHisPheGlySerAspAlaAspPheThrTrp 383  
|||:|||||  
QY 1217 GAAGTGTGTCAGGCCCTC 1234  
|||:|||||  
Db 384 GluValValLysProLeu 389  
|||:|||||

## RESULT 8

T06180

methionine adenosyltransferase (EC 2.5.1.6) - barley

N/Alternate names: S-adenosylmethionine synthetase

C/Species: Hordeum vulgare (Barley)

C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T06180

R/Mori, S.

submitted to the EMBL Data Library, August 1995

A/Reference number: Z15512

A/Accession: T06180

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-394 &lt;MOR&gt;

A/Cross-references: UNIPROT:P50299; EMBL:D63835; PIDN:BAA09895.1

C/Superfamily: methionine adenosyltransferase

C/Keywords: S-adenosylmethionine; transferase

## Alignment Scores:

Pred. No.:	5,04e-144	Length:	394
Score:	1900.50	Matches:	354
Percent Similarity:	96.16%	Conservative:	22
Best Local Similarity:	90.54%	Mismatches:	14
Query Match:	69.16%	Indels:	1
DB:	2	Gaps:	1

US-10-734-698A-38 (1-1485) x T06180 (1-394)

QY 77 GCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGC 136  
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Db 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22  
|||:|||||  
QY 137 GACCAATCTCCGATGCTCCTCGAGCTTGCCTTGAACAGGACCCAGACAGGTT 196  
|||:|||||  
Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal 42  
|||:|||||  
QY 197 GCCTCGCAACATGCACCAAGACCACTTGCTGTCATGCTTCCGAGAGATCCACCAAG 256  
|||:|||||  
Db 43 AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrLys 62  
|||:|||||  
QY 257 GCCAAGCTTGACTACGAGAGATCGTCGCTGACCTCGAGGAACTCGGCTCGCTCA 316  
|||:|||||  
Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAspIleGlyPheIleSer 82  
|||:|||||  
QY 317 AACGATGTGGACTTGATGCTGCAACTGCAAGTCTTGTAAACATTGAGCAGCAGAGC 376  
|||:|||||  
Db 83 AspAspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnGlnSer 102  
|||:|||||  
QY 377 CCTGATATTGCCAGGGTGTGCACCGCCACTTTACCAAAAGACCCGAGGAAATCGGTGCT 436  
|||:|||||  
Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysThrArgProGluGluValGlyAla 122  
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QY 437 GGAGACCGGGTCACATGTTTGGCTATGCCACGGACGAAACCCAGAAATTGATGCCATTG 496  
|||:|||||

Db 123 GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142  
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QY 497 AGTCATGTTCTTGCACAACTAAACTCGGTGCTCTCACCAGAGTTCCGAAGACGCAACC 556  
|||:|||||  
Db 143 ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162  
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QY 557 TCCCATGTTGAGGCTGATCGGAAAACCCAAAGTACTGTTGAGTATTCAATGACAAC 616  
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Db 163 CysAlaTrpLeuArgProAspGlyLysThrGlnValThrIleGluLysLeuAsnGluGly 182  
|||:|||||  
QY 617 GGTGCCATGTTCCAGTTCGTCTCCACTGTCCTATCTCCACCAACATGATGAGACT 676  
|||:|||||  
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202  
|||:|||||  
QY 677 GTGACCAACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCG 736  
|||:|||||  
Db 203 ValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIlePro 222  
|||:|||||  
QY 737 GAGAGTACCTTGTGAGAGACCACTTTTCCACTTGAACCCCTCTGGCGGTTTGTTCATT 796  
|||:|||||  
Db 223 GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242  
|||:|||||  
QY 797 GGAGGTCTCACGGTGATGCTGCTCACCAGCGCCGAGATCATCATCATCTTACCGA 856  
|||:|||||  
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrAlaArgLysIleIleAspThrTyrGly 262  
|||:|||||  
QY 857 GGATGGGTGCTCATGTTGCTGCTTCTCCGGNAGGATCCACCAAGGTTGATAGG 916  
|||:|||||  
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282  
|||:|||||  
QY 917 AGTGTGCTTACATTGTGAGACAGCTGCTAAAGACATTGTGCGAAGTCGACTAGCCAGA 976  
|||:|||||  
Db 283 SerGlyAlaTyrIleAlaArgGlnAlaLysSerIleIleAlaSerGlyLeuAlaArg 302  
|||:|||||  
QY 977 AGGTGCATTGTCGAAGTCTTATGCCATTGTGTGCCGAGCCTTGTCTGCTTTGTT 1036  
|||:|||||  
Db 303 ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322  
|||:|||||  
QY 1037 GACACTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTCTGAAGGAGAAC 1096  
|||:|||||  
Db 323 AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysValLysGluAsn 342  
|||:|||||  
QY 1097 TTTGATTTTCAGCCCGGTATGATCTCCATCAACTTGATCTCAAGAGGGGTGGGAATAAC 1156  
|||:|||||  
Db 343 PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysLysGlyGly---Asn 361  
|||:|||||  
QY 1157 AGTCTTCTGAGACCTGCTGCATATGGACACTTTCGGCAGAGAGACCCCTGACTTCATCG 1216  
|||:|||||  
Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381  
|||:|||||  
QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
|||:|||||  
Db 382 GluValValLysProLeuLysPheAspLysAla 392  
|||:|||||

## RESULT 9

S46540

methionine adenosyltransferase (EC 2.5.1.6) - tomato

N/Alternate names: S-adenosyl-L-methionine synthetase

C/Species: Lycopersicon esculentum (tomato)  
C/Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S46540; S38876

R/Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.

Plant Mol. Biol. 25, 217-227, 1994

A/Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in re-

A/Reference number: S46538; MUID:94289846; PMID:8018871

A/Accession: S46540

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-390 &lt;ESP&gt;

A/Cross-references: UNIPROT:P43282; EMBL:Z24743; NID:9429107; PIDN:CAA80867.1; PID:94291

C/Superfamily: methionine adenosyltransferase

C/Keywords: S-adenosylmethionine; transferase

## Alignment Scores:

Pred. No.: 1,05e-142 Length: 390  
Score: 1884.00 Matches: 352  
Percent Similarity: 95.34% Conservativity: 16  
Best Local Similarity: 91.19% Mismatches: 18  
Query Match: 68.56% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S46540 (1-390)

```
QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGGC 199
Db 22 GluValSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
QY 200 TCGGAACATGCACCAAGACCACTTGCTCATGCTTCGGAGAGATCACCAACGAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGGGTGACACCTGCAGGAACATCGGCTTCTCTCAAC 319
Db 62 ThrValAspTyrGluLysIleValalargaspThrCysArgGlyIleGlyPheValSerAla 81
QY 320 GATGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGCAGACCCCT 379
Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY 380 GATATTGCCAGGGTGTGACGGCCACCTTACCAAGACCCGAGGAATCGTCTCGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121
QY 440 GACCAAGGTCACATGTTTCGCTATGCCAGGACGAAACCCAGAAATTCATGTCATTGAT 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCAACTAACTCGGTGCTGCTCTCACCGAGTTCGCAAGAACGGAACCTGCG 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCys 161
QY 560 CCATGTTGAGCCCTGATCGGAAACCCAAAGTACTGTTGAGTATTACAATGACACACCGT 619
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspAsnGly 181
QY 620 GCATGTTTCCAGTTCGTCCTCACACTGTGCTTATCTCCACCAACATCATGATGAGCTGTG 679
Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAACGACGAATTGACAGTCACTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG 739
Db 202 ThrAsnAspGlnIleAlaGlnAspLeuLysGluHisValIleLysProValIleProAla 221
QY 740 AGTACTTGTAGAGAGACCAATTTTCCACTTGAACCCCTCTGCGGTTTGTCTCATTTGA 799
Db 222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTCAGGTGATGCTGCTCTCACCGCCGCGAGATCATCATCATGATCTTACCGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261
QY 860 TGGGGTCTCATGTTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GGTGCTTACATTGTGACAGGCTGCTAAGACATGTCGCAAGTGGACTACCGAGGAG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaSerGlyLeuAlaArgArg 301
QY 980 TGCATTGTCAGAGTGTCTTATGCCATTGGTGTGCGCGAGCCCTTGTCTCTTTGTTGAC 1039
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Db 302 CysIleValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerValPheValAsp 321
QY 1040 ACCTATGCGCCGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGGAGAACTTT 1099
Db 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuValLeuIleLysGluAsnPhe 341
QY 1100 GATTTCAGGCCCGGTATGATCTCCATCAACCTTCATCTCAAGAGGGGTGGGAATAACAGG 1159
Db 342 AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLeuArgGlyGlyAsnTyrArg 361
QY 1160 TTCTGAAGACTGTCATATGCACATTCGCGCAGAGAGGACCTTGATCTCACATGGGAA 1219
Db 362 TyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGGTCAGGCCCTCAAG 1237
Db 382 ThrValLysValLeuLys 387
RESULT 10
GB4785
probable s-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84785
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84785
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <STO>
A:Cross-references: UNIPROT:Q9SUL8; GB:AB002093; NID:G4883604; PIDN:AAD31573.1; GSPDB:GN
C:Genetics:
A:Gene: At2g36880
A:Map position: 2
C:Superfamily: methionine adenosyltransferase
Alignment Scores:
Pred. No.: 9.64e-142 Length: 390
Score: 1872.00 Matches: 348
Percent Similarity: 95.08% Conservativity: 19
Best Local Similarity: 90.16% Mismatches: 19
Query Match: 68.12% Indels: 0
DB: 2 Gaps: 0
US-10-734-698A-38 (1-1485) x G84785 (1-390)
QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGGC 199
Db 22 GluIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
QY 200 TCGGAACATGCACCAAGACCACTTGCTCATGCTTTCGGAGAGATCACCAACGAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrAlaAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGGGTGACACCTGCAGGAACATCGGCTTCTCTCAAC 319
Db 62 LysValAspTyrGluLysIleValargSerThrCysArgGluIleGlyPheIleSerAla 81
QY 320 GATGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGCAGACCCCT 379
Db 82 AspValGlyLeuAspAlaAspLysCysAsnValLeuValAsnIleGluGlnGlnSerPro 101
QY 380 GATATTGCCAGGGTGTGACGGCCACCTTACCAAGACCCGAGGAATCGTCTCGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluAspIleGlyAlaGly 121
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QY 440 GACACGGTCAATGTTTGGCTATGCCACGACGAAACCCAGAAATGTGATTCGCAATGAGT 499
Db 122 AspGlnGlyHisMetPheGlyTyAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCACTAACTCGGTGCTCGTCTCACCGAGGTTCGCAAGAACGCACTGC 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaLeuLeuThrGluValArgLysLeuLysThrCys 161
QY 560 CCATGGTTGAGGCTCATGGGAAACCAAGTCACTGTTGAGTATTACATCAACACGGT 619
Db 162 ProTrieuArgProAspGlyLysThrGlnValThrValGluTyLysLeuAspGlyGly 181
QY 620 GCCATGGTTCCATGTCGTGCCACATGTCCTTATCTCCACCAACCAATGATGAGACTGG 679
Db 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAACGCAATTCAGCTGACCTCAAGGACATGTCATCAAGCCGCTGATCCCGGAG 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProAla 221
QY 740 AAGTACTCTGATGAGAGACCAATTTCCACTTGAACCCCTCTGGCCGTTTGTTCATTGGA 799
Db 222 LysTyLeuAspAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCACGGTATGCTGCTCTCACCGCCGCAAGATCATCATCGATATTCACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyGlyGly 261
QY 860 TGGGGTCTCATGGTGGTGGTCTTCTCGGGAGGATCCCAAGGTGATGAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GGTGCTTACATTCGACAGAGGTGCTAAGAGCATTTGCGAGGTGCTAGCCAGAGG 979
Db 282 GlyAlaTyIleValArgGlnAlaAlaLysSerValAlaAlaGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGTCTTATGTCATTGGTGTGTCGCCGAGCCTTGTGCTGCTTGTGAC 1039
Db 302 CysIleValGlnValSerTyAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAGGAGATTCACACATGTCGAGGAGAACTTT 1099
Db 322 ThrTyLysThrGlyThrIleProAspLysAspIleLeuValLeuIleLysGluAlaPhe 341
QY 1100 GATTTCCAGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATACAG 1159
Db 342 AspPheArgProGlyMetMetAlaIleAsnLeuAspLeuLysArgGlyGlyAsnPheArg 361
QY 1160 TTCTTGAAGACTGCTCATATGACACTTCGCGAGAGAGACCCCTGACTTCATCGGAA 1219
Db 362 PheGlnLysThrAlaAlaTyGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGTCACACCCCTCAAG 1237
Db 382 ValValLysProLeuLys 387

RESULT 11
S49491
methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S49491
R:Izhaki, A.; Shoseyov, O.; Weiss, D.
A:Submitted to the EMBL Data Library, October 1994
A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A:Reference number: S49491
A:Accession: S49491
A:Molecule type: mRNA
A:Residue: 1-390 <I2H>
A:Cross-references: UNIPROT:P48498; EMBL:X82214; NID:g559505; PIDN:CAAS7696.1; PID:g5595
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase
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Alignment Scores:
Pred. No.: 1.53e-140 Length: 390
Score: 1857.00 Matches: 344
Percent Similarity: 94.81% Conservative: 21
Best Local Similarity: 89.33% Mismatches: 20
Query Match: 67.58% Indels: 0
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S49491 (1-390)
QY 80 GAGACATTCCTATTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCGATGCTGCTCTCGACCTTGCCTTGAACAGACCCAGACCAAGGTTGCC 199
Db 22 GlnValSerAspAlaIleLeuAspAlaCysLeuGluAspProGluSerLysValAla 41
QY 200 TCGAAACATGCAACCAAGACCACTTGTGTCATGCTTCGAGAGATCAACCAAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGTGTCACCTCAGACCAATCGGCTTCTCTCAAC 319
Db 62 ThrValAspTyzGluLysIleValArgAspThrCysArgGlyIleGlyPheThrSerAla 81
QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAGACCCCT 379
Db 82 AspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnSerPro 101
QY 380 GATATTGCCAGGGTGTGCACGGCCACTTACAAAAGACCCGAGGAAATCGGCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121
QY 440 GACACGGTCACTGTTGGCTATGCCACGACGAAACCCCGAATTTGATTCGATGAGT 499
Db 122 AspGlnGlyHisMetPheGlyTyAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCAACTTAACTCGTCTCGTCTCACCGAGGTTCGCAAGAACGCAACCTGC 559
Db 142 HisValTrpAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysLeuLysThrCys 161
QY 560 CCATGGTTGAGCCTGTATGGGAAACCCCAAGTGACTGTTGAGTATTACAAATCAACACGT 619
Db 162 ProTrieuArgProAspGlyLysThrGlnValThrValGluTyArgAsnAspAsnGly 181
QY 620 GCCATGGTTCCATGTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetIleProLeuArgValHisThrIleLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAACGCAATTTGCAAGTGAACCTTTCCTTCCCGGAGGATCCCAAGGTTCATAGGAGT 739
Db 202 ThrAsnAspGlnIleAlaGlnAspLeuLysGluHisValIleLysProValValProAla 221
QY 740 AAGTACTCTGATGAGAGACCAATTTCCATTTGAACCCCTCTGGCCGTTTGTTCATTGGA 799
Db 222 GluTyLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTACGGTATGCTGCTCTCACCGCCGCAAGATCATCATCGATATTCACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyGlyGly 261
QY 860 TGGGGTCTCATGGTGGTGGTCTTCTCGGGAGGATCCCAAGGTTCATAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GGTGCTTACATTCGACAGAGGTGCTAAGAGCATTTGCGAGGTGCTAGCCAGAGG 979
Db 282 GlyAlaTyIleValArgGlnAlaAlaLysSerValValAlaGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGTCTTATGTCATTGGTGTGTCGCCGAGCCTTGTGCTGCTTGTGAC 1039
Db 302 CysIleValGlnValSerTyAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAGGAGATTCACACATGTCGAGGAGAACTTT 1099
Db 322 ThrTyLysThrGlyThrIleProAspLysAspIleLeuValLeuIleLysGluAlaPhe 341
QY 1100 GATTTCCAGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATACAG 1159
Db 342 AspPheArgProGlyMetMetAlaIleAsnLeuAspLeuLysArgGlyGlyAsnPheArg 361
QY 1160 TTCTTGAAGACTGCTCATATGACACTTCGCGAGAGAGACCCCTGACTTCATCGGAA 1219
Db 362 PheGlnLysThrAlaAlaTyGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGTCACACCCCTCAAG 1237
Db 382 ValValLysProLeuLys 387
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Db 302 CysIleValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGACCGGAGATCCATATAGGAGATCTCAACATTTGTGAAGGAACTTT 1099  
Db 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuThrLeuIleGlyGluAsnPhe 341  
QY 1100 GATTTCAGGCGCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetSerIleAsnLeuAspLeuArgGlyGlyAsnPheArg 361  
QY 1160 TTCTTGAAGACTGTCATATGACATCTCGGACAGAGAGCCCTGACTTCCATGAGAA 1219  
Db 362 TyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTC 1234  
Db 382 ThrValLysValLeu 386

RESULT 12  
S66351  
methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66351  
R:Gomez-Gomez, L.; Carrasco, P.  
Plant Mol. Biol. 30, 821-832, 1996  
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries  
A:Reference number: S66351; MUID:96194463; PMID:8624412  
A:Accession: S66351  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-366 <GOM>  
A:Cross-references: UNIPROT:P49612; EMBL:X82076; NID:g609222; PIDN:CAAS57580.1; PID:g6092  
A>Note: the authors did not translate the codon for residue 1  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 3 19e-136 Length: 366  
Score: 1803.00 Matches: 341  
Percent Similarity: 95.33% Conservative: 6  
Best Local Similarity: 93.68% Mismatches: 17  
Query Match: 65.61% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S66351 (1-366)

QY 158 CTCGACGCTTGCTTGAACAGGACCCAGACAGAGGTTGCTCGCAACATGCACCAAG 217  
Db 3 ValAspAlaCysLeuGluGlnAspSerAspSerLysValAlaCysGluThrCysThrLys 22  
QY 218 ACCAACTTGGTCATGCTTCGAGAGATCACACCAAGGCCAACGTTGACTACGAGAAG 277  
Db 23 ThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLys 42  
QY 278 ATCGTCGCTGACACCTCGAGGACATCGCTTCGCTCAACAGATGTGGACTTCATGCT 337  
Db 43 IleValArgAsnThrCysArgAsnIleGlyPheValSerAlaAspValGlyLeuAspAla 62  
QY 338 GACAACTGCAAGTCTCTTGAACATTGAGCAGCAGAGCCCTGATATTGCCCGAGGTTG 397  
Db 63 AspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyVal 82  
QY 398 CACGGCCACTTACCAAAAGACCCGAGGAAATCGGTGCTGGAGACAGGTCACATGTTT 457  
Db 83 HisGlyHisPheThrLysLysProGluIleGlyAlaGlyAspGlnGlyHisMetPhe 102  
QY 458 GCGTATGCCACGACGACCCAGATTTGATGCCATTCAGTCATGCTTCGCACTAAA 517  
Db 103 GlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLys 122  
QY 518 CTCGGTGTCTGCTCACCGAGGTTCCGAAGAACCGAACCTGCCCATGTTGAGGCTGAT 577

Db 123 LeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysAlaIleTrpLeuArgProAsp 142  
QY 578 GGGAAACCCAGTGAAGTGTGACTGTATACATACAAACGGTGCATGTTCCAGTTGCT 637  
Db 143 GlyAsnThrGlnValThrValGluTyrTyrAsnAspLysGlyAlaMetValProIleArg 162  
QY 638 GTCCACACTGTGCTTATCTCCACCACATGATCAGACTGTGACCAACGACGAAATTGCA 697  
Db 163 ValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAla 182  
QY 698 GCTCACTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAGAGAGTACCTTGTATGAGAA 757  
Db 183 AlaAspLeuLysGluHisValIleLysProValIleProGluLysTyrLeuAspSerLys 202  
QY 758 ACCATTTTCCACTTGAACCCCTCTGGCGGTTTCTCATTTGGAGGTCCTCAGGTTGATGCT 817  
Db 203 ThrIleCysHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAla 222  
QY 818 GGTCTCAAGCCGCGCAAGATCATCATGATCTTACGGAGGATGGGTGCTCATGGTGGT 877  
Db 223 GlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGly 242  
QY 878 GGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGTGCTTACATTTGTGAGA 937  
Db 243 GlyAlaPheSerGlyLysAspProThrLysValAspArgArgGlyAlaTyrIleValArg 262  
QY 938 CAGCTCTAAGACATTTGGCAAGTGGACTAGCAGGAGGTCATTTGTCAGAGTGTCT 997  
Db 263 GlnAlaLysSerIleValAlaSerGlyLeuAlaArgArgAlaIleValGlnLeuLeu 282  
QY 998 TATGCCATTGGTGGCCGAGCCTTGTCTCTTTTGTGACCTATGGCACCAGGGAAG 1057  
Db 283 ArgAlaIleGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLys 302  
QY 1058 ATCCATGATAAGGAGATTTCTCAACATTGTGAAGGAGAACATTTGATTTTCAGGCCCGGTATG 1117  
Db 303 IleProAspArgGluIleLeuLysIleValLysGluThrPheAspPheArgProGlyMet 322  
QY 1118 ATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATACAGGTTCTTGAAGCATGCTGCA 1177  
Db 323 IleSerIleAsnLeuAspLeuLeuArgGlyGlyAsnGlyArgPheLeuLysThrAlaAla 342  
QY 1178 TATGGACACTTCGGCAGAGAGACCTGACATTCACATGGGAAGTGGTCAAGCCCTCAAG 1237  
Db 343 TyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLys 362

QY 1238 TGGAGAGAGGCC 1249  
Db 363 TrpGluLysAla 366

RESULT 13  
T06592  
methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-May-2000  
C:Accession: T06592  
R:Gomez, L.; Carrasco, P.  
submitted to the EMBL data library, January 1995  
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.  
A:Reference number: Z15782  
A:Accession: T06592  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-360 <GOM>  
A:Cross-references: EMBL:L36680; NID:g609556; PIDN:AAAS8772.1; PID:g609557  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 2 45e-131 Length: 360  
Score: 1742.00 Matches: 335  
Percent Similarity: 93.13% Conservative: 4  
Best Local Similarity: 92.03% Mismatches: 19

Query Match:	63.39%	Indels:	6
DB:	2	Gaps:	1
US-10-734-698A-38 (1-1485) x T06592 (1-360)			
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DB	3	ValAspAlaCysLeuGluGlnAspSerAspSerLysValAlaCysGluThrCysThrLys	22
QY	218	ACCAACTTGGTCATGCTCTTCGAGAGATCACCAAGGCCCAACCTTGACTACGAGAAG	277
DB	23	ThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLys	42
QY	278	ATCGTCGGTGACACCTCGAGGAACATCGCTCTCAACAGATGGAGACTTGATGCT	337
DB	43	IleValArgAsnThrCysArgAsnIleGlyPheValSerAlaAspValGlyLeuAspAla	62
QY	338	GACAACCTGAAGTCTCTTGAACATTGAGCAGCAGACCCCTCATATGCCAGGGTGG	397
DB	63	AspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyVal	82
QY	398	CACGGCCACCTTACCAAAAGACCCGAGAAATCGGTGCTGGAGACCAAGGTTCACATGTT	457
DB	83	HisGlyHisPheThrLysArgProGluGluIleGlyAlaGlyAspGlnGlyHisMetPhe	102
QY	458	GGCTATGCCACGGACGAACCCAGAAATTGATGCCATTGAGTCATGTTCTTGCAATAAA	517
DB	103	GlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLys	122
QY	518	CTCGGTGCTGCTCACCGAGTTCGCAAGACGGACCTGCCCATGTTGAGGCTGAT	577
DB	123	LeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysAlaThrLeuArgProAsp	142
QY	578	GGGMAAACCAAGTACTGTAGTATTACAATGACACCGGTGCCATGTTCCAGTTCGT	637
DB	143	GlyAsnThrGlnValThrValGluTyrTyrAsnAspLysGlyAlaMetValProIleArg	162
QY	638	GTCCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTGACCAACGACGAATTGCA	697
DB	163	ValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAla	182
QY	698	GCTGACCTCAAGAGCATGTGATCAAGCCGGTGATCCCGAGAGTAGTACCTTGATGAGAG	757
DB	183	AlaAspLeuLysGlyHisValIleLysProValIleProGluLysTyrLeuAspSerLys	202
QY	758	ACCATTTTCCACTTGAAACCCCTCTGGCCGTTTTGTTCATTGGAGGTCTCACGCTGATGCT	817
DB	203	ThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAla	222
QY	818	GGTCTCACCGCGCGCAAGATCATCATCTTACGAGAGATGGGGTGCTCATGCTGCT	877
DB	223	GlyLeuThrGlyArgLysIleIleAspThrTyrGlyCysThrArgCys-----	239
QY	878	GGTGCTTTCTCGGGAAGATCCACCAAGTTGTATAGAGTGGTGTTCATATTGTGAGA	937
DB	240	-----SerGlyLysAspProThrLysValAspArgArgGlyValatyrIleValArg	256
QY	938	CAGGCTGCTTAAGAGCATTGTGGCAAGTGGACTAGCCAGAGGTGCAATTCGCAAGTGCT	997
DB	257	GlnAlaAlaLysSerIleValIaSerGlyLeuAlaArgArgAlaIleValGlnValSer	276
QY	998	TATGCCATTGGTGTGCCGAGCCTTTGTCTGTTTGTGTTGACACCTATGGCACCGGAAG	1057
DB	277	TyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLys	296
QY	1058	ATCCATGATAGGAGATTCTCAACATGTGAGAGGAACCTTTGATTTTCAAGCCCGGTATG	1117
DB	297	IleProAspArgGluIleLeuLysIleValLysGluThrPheAspPheArgProGlyMet	316
QY	1118	ATCTCCATCAACTTCATCTCAAGAGGGGTGGGAATAACAGAGTCTCTTGAAGACTGCTGCA	1177
DB	317	IleSerIleAsnLeuAspLeuArgGlyGlyAsnGlyArgPheLeuLysThrAlaAla	336

QY	1178	RTATGACACTTCGGCAGAGAGACCCCTGACTTCACATCGGGAAGTGGTCAAGCCCTCAAG	1237
DB	337	TyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLys	356
QY	1238	TGGGAGAAGGCC	1249
DB	357	TrpGluLysAla	360
RESULT 14			
S27257			
methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human			
N/Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine syn-			
C/Species: Homo sapiens (man)			
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004			
C/Accession: S27257			
R/Horikawa, S.; Tsukada, K.			
FEBS Lett. 312, 37-41, 1992			
A/Title: Molecular cloning and developmental expression of a human kidney S-adenosylmet			
A/Reference number: S27257; MUID:93050159; PMID:1426236			
A/Accession: S27257			
A/Status: preliminary			
A/Molecule type: mRNA			
A/Residues: 1-395 <HOR>			
A/Cross-references: UNIPROT:P31153; EMBL:X68036; GB:S47059; NID:g36326; PIDN:CAA48726.1.			
C/Genetics:			
A/Gene: GDB:MAT2A; SAMS2; MATA2			
A/Cross-references: GDB:136213; OMIM:601468			
A/Map position: 2p11.2-2p11.2			
A/Introns: 15/2; 256/3			
C/Complex: heterodimer of catalytic alpha and regulatory beta chains			
C/Function:			
A/Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyro			
A/Pathway: one-carbon metabolism			
C/Superfamily: methionine adenosyltransferase			
C/Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism;			
F/279-286/Region: nucleotide-binding motif A (P-loop) #status atypical			
F/31/Binding site: magnesium 2 (Asp) #status predicted			
F/285,289/Active site: Lys #status predicted			
F/291/Binding site: magnesium 1 (Asp) #status predicted			
Alignment Scores:			
Pred. No.:	3,11e-97	Length:	395
Score:	1316.50	Matches:	254
Percent Similarity:	78.50%	Conservative:	49
Best Local Similarity:	65.80%	Mismatches:	76
Query Match:	47.91%	Indels:	7
DB:	1	Gaps:	3
US-10-734-698A-38 (1-1485) x S27257 (1-395)			
QY	83	ACATTCTCTATTACCTCAGATCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGACCAA	142
DB	17	ThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspIleCysAspGln	36
QY	143	ATCTCCGATGTGCTCTGACGCTTGGCTTGAACAGGACCCAGACAGCAAGTTGCTGCTGC	202
DB	37	IleSerAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValaCys	56
QY	203	GAACATGCCACCAAGACCAACTTGGTCATGCTTCGAGAGATCACCACCAAGGCCAAC	262
DB	57	GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla	76
QY	263	GTTGACTACGAGAAGATCGTGGTGCACACCTGCAGAAACATCGGCTTCTCTCAACCGAT	322
DB	77	ValAspTyrGlnLysValValArgGluAlaValLysHisIleGlyTyrAspAspSerSer	96
QY	323	GTGGACTTGTAGCTGACAACTGCAAGGTCTCTTGAACATTTGACAGCAGACCCCTGAT	382
DB	97	LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnGlnSerProAsp	116
QY	383	ATTCGCCAGGTGTGCACGGCCACTTACCAAGACCCGAGGAATCGTCTCGGAGAC	442
DB	117	IleAlaGlnGlyVal-----HisLeuAspArgAsnGluGluAspIleGlyAlaGlyAsp	134

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QY 443 CAGGGTCACATCTTTGGCTATGCCCGAGGAAACCCAGATTGATGCCATTGAGTCAT 502
Db 135 GlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluCysMetProLeuThrIle 154
QY 503 GTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTCGCAAGAACGGAACCTGCCCA 562
Db 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174
QY 563 TGGTTGAGCCTGATGGGAAACCCCAAGTACTGTTGAGTATTACAATGACAAACGGTGCC 622
Db 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194
QY 623 ATGGTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACATGATGAGTACTGTGACC 682
Db 195 ValLeuProIleArgValHisThrIleValIleSerValGlnHisAspGluValCys 214
QY 683 AACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCCGTGATCCCGGAGAAG 742
Db 215 LeuAspGluMetArgAspAlaLeuLysGluLysValIleLysAlaValProAlaLys 234
QY 743 TACCTTGATGAGAAGACCAATTTCCATTGAACCCCTCTGGCCGTTTGTCTATTGGAGGT 802
Db 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254
QY 803 CCTCAGGTGATGCTGCTCTCACCGCCGCAAGATCATCATCATGATGATGAGGATGG 862
Db 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleValIleValAspThrTyrGlyGlyTyr 274
QY 863 GGTGCTCATGCTGCTGCTCTTCTCCGGGAAGGATCCCAAGGCTTGTGATGAGGATGCT 922
Db 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294
QY 923 GCTTACATTTGTGAGACAGCTGCTTAAGACATTGTGGCAAGTGGACTAGCCAGAGGTGC 982
Db 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLeuCysArgVal 314
QY 983 ATTTGTCAGTCTCTATCCCATCTGCTGTCGCCGAGCTTCTGCTCTTCTTGTGCACACC 1042
Db 315 LeuValGlnValSerTyrAlaIleGlyValSerHisProLeuSerIleSerIlePheHis 334
QY 1043 TATGGCACCGGAAGATCCATGATAGGAGATTCTCAACATTTGTGAAGAGAACTTTGAT 1102
Db 335 TyrGlyThrSerGlnLysSerGluArgGluLeuLeuGluIleValLysLysAsnPheAsp 354
QY 1103 TTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACAGGTTC 1162
Db 355 LeuArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProIleTyr 371
QY 1163 TTGAAGACCTGTCATCGACATCGACATTCGGCAGAGAGCCCTGACTTCACATGGGAAGTG 1222
Db 372 GlnArgThrAlaAlaTyrGlyHisPheGlyArgAsp-----SerPheProTrpGluVal 389
QY 1223 GTCAAGCCCTCAAGTGG 1240
Db 390 ProLysLysLeuLysTyr 395
RESULT 15
A37118
methionine adenosyltransferase (EC 2.5.1.6) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 09-Jul-2004
C:Accession: A37118
R:Horikawa, S.; Saeuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney s-ade
A:Reference number: A37118, MUID:90337979, PMID:1696256
A:Accession: A37118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <ROR>
A:Cross-references: UNIPROT:P182298; GB:J05571; NID:g206845; PID:AAA42106.1; PID:g206846
C:Superfamily: methionine adenosyltransferase
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C:Keywords: S-adenosylmethionine; transferase

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Alignment Scores:          9.41e-97          Length:          395
Pred. No.:                1310.50          Matches:         251
Score:                    78.24%          Conservative:    51
Percent Similarity:       78.24%          Mismatches:     77
Best Local Similarity:    65.03%          Indels:         7
Query Match:              47.69%          Gaps:          3
Db:
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US-10-734-698A-38 (1-1485) x A37118 (1-395)

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QY 83 ACATTCTATTACTCAGAGTCAGTGAACGAGGGACACCCCTGACAAGCTCTGGACCAA 142
Db 17 ThrPheLeuPheThrSerGluSerValGlyGluHisProAspLysIleCysAspGln 36
QY 143 ATCTCCGATGCTGCTCTGACGCTTGGCTTGAACAGACCCAGACAGCAAGTTGCTTCG 202
Db 37 IleAsnAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValAlaCys 56
QY 203 GAAACATGCACCAAGACCACTTGGTCATGCTCTCGAGAGATCACCACCAGGCCAAC 262
Db 57 GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla 76
QY 263 GTTGACTACGAGAAGATCGTCGTGACACCTCGCAGGAACATCGGCTTCTCTCAACCAT 322
Db 77 IleAspTyrGlnLysValValArgGluAlaIleLysHisIleGlyTyrAspAspSerSer 96
QY 323 GTGGACTTGTGATGTCACAACTGCAAGGTCTTGTAAACATGTGAGCAGCAGACCTTGAT 382
Db 97 LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnGlnSerProAsp 116
QY 383 ATTCGCCAGGTGTGCACGGCCACTTACCAAAAGACCCGAGGAATCGGTCTGGAGAC 442
Db 117 IleAlaGlnGlyVal-----HisLeuAspArgAsnGluGluAspIleGlyAlaGlyAsp 134
QY 443 CAGGTCACATGTTTGGCTATGCCACGACCAAAACCCAGAAATGTATGCCATTGAGTCAT 502
Db 135 GlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluGluCysMetProLeuThrIle 154
QY 503 GTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTCGCAAGAACGGAACCTGCCCA 562
Db 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174
QY 563 TGGTTGAGCCTGATGGGAAACCCCAAGTACTGCTGAGTATTACAATGACAAACGGTGCC 622
Db 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194
QY 623 ATGGTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACATGATGAGACTGTGACC 682
Db 195 ValIleProIleArgValHisThrIleValIleSerValGlnHisAspGluValCys 214
QY 683 AACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCCCGTGATCCCGGAGAAG 742
Db 215 LeuAspGluMetArgAspAlaLeuLysGluLysLeuIleLysAlaValProAlaLys 234
QY 743 TACCTTGATGAGAAGACCAATTTCCATTGAACCCCTGCTGCGCTTTTGTCTATTGGAGGT 802
Db 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254
QY 803 CCTCAGGTGATGCTGCTCTCACCGCCGCAAGATCATCATCATGATGAGTACTGTGACC 862
Db 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleValIleValAspThrTyrGlyGlyTyr 274
QY 863 GGTGCTCATGCTGCTGCTCTTCTCCGGGAAGGATCCCAAGGCTTGTGATGAGGATGCT 922
Db 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294
QY 923 GCTTACATTTGTGAGACAGCTGCTTAAGACATTGTGGCAAGTGGACTAGCCAGAGGTGC 982
Db 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLeuCysArgVal 314
QY 983 ATTTGTCAGTCTCTATCCCATCTGCTGTCGCCGAGCTTCTGCTCTTGTGTGCACACC 1042
```



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 17:02:27 ; Search time 276.5 Seconds  
(without alignments)  
5500.453 Million cell updates/sec

Title: US-10-734-698A-38

Perfect score: 2748  
Sequence: 1 AGCCAGGCCCACTCAACCA.....CAAAAGAAATGTTCCAAGTT 1485

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DRV=xlp  
-Q/cn2\_1/USPTO spool\_p/US10734698/runat\_25082005\_105400\_10267/app\_query.fasta\_1.1671  
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10734698 @CN1\_1\_307 @runat\_25082005\_105400\_10267 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DRV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_treml:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	74.1	392	Q8W3Y4	Q8W3Y4 phaseolus 1
2	2007	73.0	391	Q6J9X6	Q6J9X6 medicago sa
3	2003	72.9	393	1 METK_CATRO	Q96551 catharanthu
4	2003	72.9	393	1 METK_CATRO	Q96552 catharanthu
5	1993	72.5	393	2 Q9AT55	Q9at55 elaeagnus u
6	1992	72.5	393	2 Q9AT56	Q9at56 elaeagnus u
7	1989	72.4	395	1 METK_POPDE	P47916 populus del
8	1986	72.3	393	2 Q84NM2	Q84nm2 lichl chin
9	1985	72.2	393	1 METK_LYCES	P43280 lycopersico
10	1983	72.2	393	1 METK_LYCES	P43281 lycopersico
11	1979	72.0	393	2 Q9SBQ7	Q9sbq7 petunia hyb
12	1974.5	71.9	395	2 Q944U4	Q944u4 dendrobium
13	1972.5	71.8	429	2 Q8GTL5	Q8gtl5 carica papa
14	1968	71.6	393	2 Q6GV10	Q6gv10 solanum bre
15	1960	71.3	393	2 Q9FUZ1	Q9fuz1 brassica ju
16	1959	71.3	395	2 Q9FPL6	Q9fpl6 suaeda saia

17	1957.5	71.2	394	1 METL_ORYSA	P93438 oryza sativ
18	1957.5	71.2	394	2 Q7F660	Q7f660 oryza sativ
19	1953	71.1	396	1 METK_ORYSA	P46611 oryza sativ
20	1953	71.1	396	2 Q6AVZ2	Q6avz2 oryza sativ
21	1952	71.0	393	2 Q94FA4	Q94fa4 brassica ju
22	1949	70.9	396	2 Q8VXC5	Q8vxc5 oryza sativ
23	1949	70.9	396	2 Q9LGU6	Q9lgue oryza sativ
24	1948.5	70.9	396	2 Q6F3F0	Q6f3f0 atriplex nu
25	1947	70.9	393	1 METL_ARATH	P17562 arabidopsis
26	1940.5	70.6	392	1 METK_MESCR	P93254 mesembryant
27	1940	70.6	393	1 METK_ARATH	P23586 arabidopsis
28	1940	70.6	393	2 Q94FA6	Q94fa6 brassica ju
29	1939.5	70.6	396	2 Q6F3F1	Q6f3f1 atriplex nu
30	1938	70.5	393	2 Q9LDQ7	Q9ldq7 camellia si
31	1935.5	70.4	396	2 Q6F3F4	Q6f3f4 atriplex nu
32	1935	70.4	393	2 Q9LUT2	Q9lut2 arabidopsis
33	1932.5	70.3	396	1 METL_DIACA	P24260 dianthus ca
34	1932	70.3	393	1 METK_BRAJU	P49611 brassica ju
35	1931.5	70.3	393	1 METK_MUSAC	O22338 musa acumin
36	1930.5	70.3	396	2 Q7XZR1	Q7xzi1 atriplex nu
37	1926.5	70.1	396	2 Q6F3F3	Q6f3f3 atriplex nu
38	1907	69.4	393	1 METK_PINBN	P50300 pinus banks
39	1906	69.4	393	2 Q9FVG7	Q9fvg7 pinus conto
40	1900.5	68.2	394	1 METM_HORVU	P50299 hordeum vul
41	1884	68.6	390	1 METM_LYCES	P43282 lycopersico
42	1872	68.1	390	2 Q9S7L8	Q9s7l8 arabidopsis
43	1869	68.0	390	2 Q9M7K8	Q9m7k8 nicotiana t
44	1866	67.9	390	2 Q94FA5	Q94fa5 brassica ju
45	1857	67.6	390	1 METK_PETHY	P48498 petunia hyb

#### ALIGNMENTS

RESULT 1  
Q8W3Y4 PRELIMINARY; PRT; 392 AA.  
AC Q8W3Y4;  
DT 01-MAR-2002 (TREMELrel. 20, Created)  
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE S-adenosylmethionine synthetase.  
GN Name=SAMS;  
OS Phaseolus lunatus (lima bean) (Phaseolus limensis).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3884;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22056020; PubMed=12060229;  
RA Arimura G., Ozawa R., Nishioka T., Boland W., Koch T., Kuhnemann F.,  
RA Takabayashi J.;  
RT "Herbivore-induced volatiles induce the emission of ethylene in  
neighboring lima bean plants.";  
RL Plant J. 29:87-98(2002).  
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine +  
diphosphate + S-adenosyl-L-methionine.  
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -!- PATHWAY: Activated methyl cycle.  
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
DR EMBL; AB062358; BAB83761.1; -;  
DR HSSP; P13444; 1QM4.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
DR Pfam; PF00438; S-AdoMet\_synt\_N; 1.

DR PIRSF: PIRSF000497; MAT: 1.  
 DR TIGRFAMS; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transference.  
 SQ SEQUENCE 392 AA; 43060 MW; 9F4CA2CAAD240209 CRC64;

Alignment Scores:  
 Pred. No.: 2,17e-149 Length: 392  
 Score: 2035.00 Matches: 384  
 Percent Similarity: 98.72% Conservativity: 3  
 Best Local Similarity: 97.96% Mismatches: 5  
 Query Match: 74.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-734-698a-38 (1-1485) x Q8W3Y4 (1-392)

QY 74 ATGGCAGAGACATTCCTATTACCTCAGAGTCAAGGAGGACACCCCTGACAGCTC 133  
 Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLeu 20  
 QY 134 TCGCACCACAAATCCGATGCTCTCTCGACGCTTCGCTTGAACAGGACCCAGACGAAG 193  
 Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLys 40  
 QY 194 GTTGCTGCGAAACATGACCAAGACCAACTGCTGTCATGCTTCGGAGAGATCACACC 253  
 Db 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 60  
 QY 254 AAGGCCAACGTTGACTTACGAGAGATCGTCTGACCTGACCTGACGAGAACATCGCTTCGTC 313  
 Db 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIle 80  
 QY 314 TCAACAGATGTGGACTTGATGCTGACAACTCAAGGTCCTTGTAAACATTTGACGACGAG 373  
 Db 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100  
 QY 374 AGCCCTGATTTGCCAGGGTGTGCACGGCCACCTTACAAAGACCCGAGGAATCGGT 433  
 Db 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120  
 QY 434 GCTGGAGACCGGTCACATGTTTGGCTATGTCACGAGCAAGAACCCCAAGATTTGATGCA 493  
 Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140  
 QY 494 TTGAGTCATGTTCTTGCAACTAACTCGGTGCTCGTCTCACCGAGGTTGCAAGAACGGA 553  
 Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160  
 QY 554 ACTGCGCATGTTGAGGCTGATGGGAAACCCAGTGACTGTTGAGTATTACATGAC 613  
 Db 161 ThrCysSerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAsp 180  
 QY 614 AACGGTGCCATGTTCCAGTTCGTGCCACTGTCTTATCTCCACCCCAACATCATGAG 673  
 Db 181 LysGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200  
 QY 674 ACTGTGACCAACGAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 733  
 Db 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220  
 QY 734 CCGGAGAAGTACTTGATGAGAGACCATTTCCACTTGAACCCCTCGGCCGTTTGTTC 793  
 Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240  
 QY 794 ATTGAGGTCCTCACGGTCATGCTGCTCACCGCGCAGATCATCATCATCTTAC 853  
 Db 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260  
 QY 854 GGAGGATGGGGTCTCATGGTGGTGGTCTTTCTCGGGAAGGATCCCAACCAAGTTGAT 913  
 Db 261 GlyGlyTrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280

QY 914 AGGAGTGTGCTTACATTTGTGAGACAGCTGCTAAGAGCATTGTGCAAGTGGACTAGCC 973  
 Db 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGluLeuAla 300  
 QY 974 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCCTTTCTGTCTTT 1033  
 Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320  
 QY 1034 GTTGACACCTATGGCAGCGGAGATCATCATTAAGAGATTTCTCAACATTTGTAAGGAG 1093  
 Db 321 ValAspThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGlu 340  
 QY 1094 AACTTGTATTTCCAGCCCGGTATGATCTCCATCACTTGTGATCTCAAGAGGGTGGGAAT 1153  
 Db 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyLysAsn 360  
 QY 1154 AACAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGACCCCTGACTTCACA 1213  
 Db 361 SerArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380  
 QY 1214 TGGGAAGTGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 381 TrpGluValValLysProLeuLysTrpGluLysAla 392

RESULT 2

QY Q6J9X6 PRELIMINARY; PRT; 391 AA.  
 AC Q6J9X6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE S-adenosylmethionine synthase (Fragment).  
 OS Medicago sativa (Alfalfa).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 ON NCBI\_taxID=3879;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheng R.M., Carbajal L., Potenza C., Bagga S., Sengupta-Gopalan C.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 methionine and ATP (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 DR EMBL; AY560003; AY40304.1; -. IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferrase activity; IEA.  
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF02773; S-AdoMet\_synth\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth\_M; 1.  
 DR Pfam; PF00438; S-AdoMet\_synth\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMS; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transference.  
 FT NON TER 391 391  
 SQ SEQUENCE 391 AA; 42805 MW; 0A1DB416F59CDBCF CRC64;

Alignment Scores:  
 Pred. No.: 3.26e-147 Length: 391  
 Score: 2007.00 Matches: 379  
 Percent Similarity: 97.95% Conservativity: 3

Best Local Similarity: 97.18% Mismatches: 8  
 Query Match: 73.03% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-734-698a-38 (1-1485) x Q6J9X6 (1-391)

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACCCCTGACAGCTCTCGAC 139  
 DB 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCACGACGACGAGTTGCC 199  
 DB 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspValAspSerLysValAla 41  
 QY 200 TCGAAACATGCAACAGACCACTTGGTCATGCTCTCGGAGAGATCACCCACCAAGGCC 259  
 DB 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
 QY 260 AACGTTGATCAGAGAAGATCGTGTGACACCTGAGGAAACATCGGCTTGTCTCAAC 319  
 DB 62 LysValAspTyrGluLysIleValArgAspThrCysArgLysIleGlyPheValSerAsp 81  
 QY 320 GATGTGGGATGATGCTGACACTGCAAGTCTTGTAAACATTCAGCAGCAGACCCCT 379  
 DB 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
 QY 380 GATATTGCCAGGCTGTGACGCGCCACCTTACCAAGAGACCCGAGGAAATCGGTGCGA 439  
 DB 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
 QY 440 GACAGGGTCATGTTGGCTATGCCACGAGCAACCCCAAGAAATGTATGTCATTGAT 499  
 DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCACAACTCGTGTCTCTCACCGAGGTCGCAAGAACCGACCTGCG 559  
 DB 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
 QY 560 CCATGTTGAGGCTGATGGGAAACCCCAAGTCACTGTTGAGTATTACATGACACAGCT 619  
 DB 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyraAsnAspGly 181  
 QY 620 GCATGTTCCAGTTCGTCACACTGCTGCTTATCTCCACCAACATGATGAGCTG 679  
 DB 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCACGAGAAATTCACCTGACCTCAGGAGCATGTCATCAAGCGGTGATCCGGAG 739  
 DB 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 221  
 QY 740 AAGTACCTTGATGAGAGACCACTTTCCACTTGAACCCCTCTGGCGTTTGTCTGATTGA 799  
 DB 222 LysTyrLeuAspSerLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GTCTCTCAGGTGATGCTGCTTCCACCGCCGCAAGATCATCATGATATCTACGAGGA 859  
 DB 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
 QY 860 TGGGGTGTCTCATGGTGTGCTGCTTCTCCGGAGGATCCACCAAGTTGATAGAGT 919  
 DB 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GTGCTTACATGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGCATACCGAAGG 979  
 DB 282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArg 301  
 QY 980 TGCATTGTCAGAGTCTTATGCCATTTGTCGCCGAGCCCTTGTCTGCTTGTGAC 1039  
 DB 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
 QY 1040 ACCTATGGACCGGAGAGATTCATGATAGGAGATCTCAACATTTGTGAGGAGACTTT 1099  
 DB 322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGlnAsnPhe 341

RESULT 3

METK CATRO  
 ID METK CATRO STANDARD; PRT; 393 AA.  
 AC Q96551;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 1) (AdoMet synthetase 1).  
 GN Name=SAMS1;  
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;  
 OC Catharanthus.  
 OX NCBI\_TaxID=4058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9718855; PubMed=9037140; DOI=10.1023/A:1005711720930;  
 RA Schroeder G., Eichel J., Breinig S., Schroeder J.;  
 RT "Three differentially expressed S-adenosylmethionine synthetases from  
 Catharanthus roseus: molecular and functional characterization.";  
 RL Plant Mol. Biol. 33:211-222(1997).  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 methionine and ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Z71271; CA95956.1; -.  
 DR HSSP; P13444; 1QM4.  
 DR InterPro; IPR002133; S-AdoMet\_synt.  
 DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
 DR Pfam; PF04368; S-AdoMet\_synt\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
 DR ATP-binding; Magnesium; Metal-binding; Multigene family;  
 KW One-carbon metabolism; Potassium; Transferase.  
 FT NP\_BIND 119 124 ATP (Potential).  
 FT METAL 17 17 Magnesium (By similarity).  
 FT METAL 43 43 Potassium (By similarity).  
 FT METAL 271 271 Potassium (By similarity).  
 FT METAL 279 279 Magnesium (By similarity).  
 FT BINDING 147 147 ATP (Potential).  
 SQ SEQUENCE 393 AA; 43050 MW; 04371F2B55BE386F CRC64;

## Alignment Scores:

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Pred. No.: 6,69e-147 Length: 393
Score: 2003.00 Matches: 374
Percent Similarity: 98.72% Conservative: 11
Best Local Similarity: 95.90% Mismatches: 5
Query Match: 72.89% Indels: 0
DB: 1 Gaps: 0

US-10-734-698A-38 (1-1485) x METL_CATRO (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGCACCTCGACAAGCTCTCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCGATGCTGCTCGACGCTTCGCTTGAACAGGACCCAGACAGAGGTTGCG 199
Db 22 GinIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41
QY 200 TCGCAACATGCACCAAGACCAACTTGGTCATGCTTCGCGAGAGATCACCAAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluLeuThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAACATCGGCTTCGCTCAAC 319
Db 62 ThrValAspTyRGlulysIleValArgAspThrCysArgSerIleGlyPheValSerAsp 81
QY 320 GATGCGGACTGATGCTGACAACTGCAAGGCTCTTGTAAACATTTGAGCAGCAGAGCCCT 379
Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY 380 GATATTGCCAGGCTGTCACCGCCACCTTACCAAGACCCGAGGAATCGGCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121
QY 440 GACGAGGTCACATGTTTGGCTATGCCAGCAGCAAAACCCAGAAATTTGATGCTATTGAT 499
Db 122 AspGlnGlyHisMetPheGlyTyRAlaThrAspGluThrProGluPheMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAACTCGGTGCTGCTCACCAGAGTTTCGCAAGAACCGAACCCTGC 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
QY 560 CATGTTGTCAGCCTGATCGGAAACCCCAAGTACTGTTGAGTATTACAAATCACACGCT 619
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyRTrpAsnGluAsnGly 181
QY 620 GCCATGGTTCAGTTCGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetValProValArgValHisThrValIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGAAATTCAGCTGACCTCAGGAGCATGTGATCAAGCCGTGATCCGGAG 739
Db 202 ThrAsnAspGlnIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 221
QY 740 AAGTACTCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGCGCTTTGCTCATTTGA 799
Db 222 LysTyLLeuAspGluValGluThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GTCTCTCACGGTGATGCTGCTCTCACCGCCGCGCAAGATCATCATGACTTTACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgGlyIleIleAspThrTyRThrGlyGly 261
QY 860 TGGGTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GTGCTTACATTTGAGACAGGCTGCTTAAGAGCATTGTGCGCAAGTGACTACCGAAGG 979
Db 282 GlyAlaTyRLeuValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
QY 980 TGCATTGTCAGTGTCTTATGCAATTTGCTGTCGCCGAGCCCTTGTCTCTTTGTCAC 1039
Db 302 CysIleValGlnValSerTyRAlaIleGlyValProGluProLeuSerValPheValAsp 321

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QY 1040 ACCTATGCGCCCGGAGAGATCCATGATAAGGAGATTCTACATTTGTGAAGGAACTTT 1099
Db 322 ThrTyRThrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341
QY 1100 GATTTCAAGCCCGGTATGATCTCCATCAACCTTGATCTCTCAAGAGGGTGGGAATAACAGG 1159
Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuLysArgGlyGlySerGlyArg 361
QY 1160 TTCTTGAAGACTGCTGCATATGACATTCGCGAGAGAGAGCCCTGACTTCACATGGGAA 1219
Db 362 PheLeuLysThrAlaAlaTyRThrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381
QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAGGCC 1249
Db 382 ValValLysProLeuLysTrpGluLysAla 391

RESULT 4
METL_CATRO STANDARD; PRT; 393 AA.
ID METL_CATRO
AC Q96552;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (AdoMet synthetase 2).
GN Name=SAMS2;
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;
OC Catharanthus
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97188555; PubMed=9037140; DOI=10.1023/A:1005711720930;
RA Schroeder G., Eichel J., Breinig S., Schroeder J.;
RT "Three differentially expressed S-adenosylmethionine synthetases from
RT Catharanthus roseus: molecular and functional characterization.";
RL Plant Mol. Biol. 33:211-222(1997).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (by similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL; 271272; CAA95857.1; -.
DR HSSP; P13444; 1QW4.
DR InterPro; IPR002133; S-AdoMet synt.
DR Pfam; PF02773; S-AdoMet synt_C; 1.
DR Pfam; PF02772; S-AdoMet synt_M; 1.
DR Pfam; PF04438; S-AdoMet synt_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
DR ATP-binding; Magnesium; Metal-binding; Multigene family;
KW One-carbon metabolism; Potassium; Transferrase.
FT NP_BIND 119 124 ATP (Potential).
FT METAL 17 17 Magnesium (by similarity).
FT METAL 43 43 Potassium (by similarity).
FT METAL 271 271 Potassium (by similarity).

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FT METAL 279 279 Magnesium (By similarity).  
 SQ BINDING 147 147 ATP (Potential).  
 ST SEQUENCE 393 AA; 43004 MW; 4A9070FB5B9B783D CRC64;

## Alignment Scores:

Pred. No.: 6,59e-147 Length: 393  
 Score: 2003.00 Matches: 376  
 Percent Similarity: 98.71% Conservative: 8  
 Best Local Similarity: 96.66% Mismatches: 5  
 Query Match: 72.89% Indels: 0  
 DB: 1 Gaps: 0

US-10-734-698A-38 (1-1485) x METL\_CATRO (1-393)

QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACAGGAGACACCTGACAGCTCTCGGAC 139  
 Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCGATGCTCTCTCGAGGCTTGCTTGAACAGGACCCAGACAGCAAGGTGCC 199  
 Db 22 GinileSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluSerLysValAla 41  
 QY 200 TCGAAACATGCACCAAGACCACTTGGTCATGCTCTCGAGAGATCCACCAAGGCC 259  
 Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
 QY 260 AAGCTTGACTACGAGAAATCGTGCCTGACACCTGCGAGGAACATCGCTCTCAAC 319  
 Db 62 GlnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
 QY 320 GATGTGGACTGATCTGACAACTGCAAGTCTTGTAAACATTCAGGACGAGACCTCT 379  
 Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
 QY 380 GATATTGCCAGGCTGTCAGGCCACCTTACCAGAACCCGAGGAATTCGTCGTGA 439  
 Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluIleGlyAlaGly 121  
 QY 440 GACCAGGGTCACATGTTTGGCTATGCCAGGAGCAACCCAGAAATTCGATTCAGT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCAACTAACTCGTGTCTCTCACCAGGTTTCGCAAGAACGACCTGC 559  
 Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
 QY 560 CCATGTTGAGGCTGATCGGAAACCCAGTCACTGTTGAGTATTACAAATCACAACGGT 619  
 Db 162 ProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 181  
 QY 620 GCCATGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCAACATCATGAGACTGTG 679  
 Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACAACGACGAATTCACACTGACCTCAAGAGAGATGTCATCAAGCCGCTGATCCCGAG 739  
 Db 202 ThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValValProGlu 221  
 QY 740 AAGTACCTTGATCAGAGACCACTTTCCACTTGCACCCCTCGCGTTTCTCATTCGA 799  
 Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GGTCTCTCAGGTCATGCTGCTCTCACCGCCGCGCAAGATCATCATCATTCACGAGGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThrGlyGly 261  
 QY 860 TGGGTGCTCATGTCGTGGTGTCTTCTCCGGAAGGATCCCAACCAAGTTCATAGGAGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GGTCTTACATTCGTGAGAGAGCTGTAGAGCATTCGCAAGTGGACCTACCAAGG 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301

QY 980 TGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCTTTGTCTCTTGTGTGAC 1039  
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 QY 1040 ACCTATGCCACCGGAGAGATCCATGATTAAGAGATCTCAACATTTGTGAGGAGACTTT 1099  
 Db 322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysValLysGluAsnPhe 341  
 QY 1100 GATTTTCAGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
 Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuLysArgGlyGlyAsnSerArg 361  
 QY 1160 TTCTTGAAGACTGTGCATATGGACATTCGCGAGAGAGCCCTGACTTCACATGGGAA 1219  
 Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 381  
 QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
 Db 382 ValValLysProLeuLysPheGluLys 390

RESULT 5  
 Q9AT55 PRELIMINARY; PRT; 393 AA.  
 AC Q9AT55;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE S-adenosyl-L-methionine synthetase (EC 2.5.1.6).  
 GN Name=SAMS2;  
 OS Elaeagnus umbellata (Autumn olive).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
 OX NCBI\_TaxID=43233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Root module;  
 RA Lee S., An C.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC EMBL; AF346306; AAK29410.1; -.  
 DR HSP; P13444; 1QM4.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO; GO:0036740; F:transferase activity; IEA.  
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF02773; S-AdoMet\_synth\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth\_M; 1.  
 DR Pfam; PF00438; S-AdoMet\_synth\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transferase;  
 SQ SEQUENCE 393 AA; 43136 MW; CCF8237D70415D4C CRC64;

Alignment Scores:  
 Pred. No.: 4.01e-146 Length: 393  
 Score: 1993.00 Matches: 371  
 Percent Similarity: 98.46% Conservative: 12  
 Best Local Similarity: 95.37% Mismatches: 6  
 Query Match: 72.53%

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DB: 2 Gaps: 0
US-10-734-698A-38 (1-1485) x Q9AT55 (1-393)
QY 80 GAGACATTCTATTATACCTCAGAGTGAACGAGGGACACCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspAspLeuCyAsp 21
QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGCG 199
Db 22 GlnIleSerAspAlaValLeuAspAlaCyLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGGAACATGCACCAAGACCACTTGGTCATGGCTTCGAGAGATCACCAACCAAGGCC 259
Db 42 CysGluThrCysSerLysThrAenMetValPheGlyGluLeuThrThrLysAla 61
QY 260 AAGCTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAACATCGCTTCTCTCAAC 319
Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgThrIleGlyPheValSerAsp 81
QY 320 GATGTGGACTGATCTGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGAGACGCT 379
Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY 380 GATATTGCCAGGCTGTGCACGCCACCTTACCAGAAAGACCCGAGGAATCGTGCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121
QY 440 GACCAAGGTCACATGTTGGCTATGCCAGCGACGAAACCCCAAGAAATTTGATGCTTGA 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAACTCGTGCTGCTCTCACCGAGGTTCGCAAGAACCACTGCG 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAspGlyThrCys 161
QY 560 CATGTTGTCAGGCTCATCGGAAACCCCAAGTACTGTTGAGTATTACATACACACGCT 619
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAspLysGly 181
QY 620 GCCATGGTTCAGTTCGTCTGCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGAAATTCACCTGACCTCAAGGACATGTCATCAAGCCGTGATCCCGAG 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValValProGlu 221
QY 740 AAGTACCTTGATGAGAAGACCACTTTTCCACTTGAACCCCTCTGCGCTTTGCTCATTTGA 799
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTCAGCGTGATGCTGCTCTCACCGCCGCAAGATCATCATCATCTTACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261
QY 860 TGGGTGCTCATGCTGCTGCTGCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GTGCTTACATTTGAGACAGCGCTGCTAAGACATTGTGGCAAGTGGACTAGCCAGAGG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGCTTATGCCATTGCTGCTGCCGAGCCTTTGCTGCTCTTTGTCAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProAspProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGAGAGATCATGATAGGAGATCTCAACATTTGTGAGGAGAACTTT 1099
Db 322 SerTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341
QY 1100 GATTTTCAGGCGCGGTATGATCTCCATCACTTGATCTCAAGAGGGGTGGGAATAACAGG 1159
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Db 342 AspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGlyGlyAsnAspArg 361
QY 1160 TTCTTGAAGACTGCTGCATATGCACATTCGCGAGAGAGGACCTTGACTTCACATGGGAA 1219
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAG 1246
Db 382 IleValLysProLeuLysTrpGluLys 390
RESULT 6
Q9AT56 PRELIMINARY; PRT; 393 AA.
ID Q9AT56;
AC Q9AT56;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosyl-L-methionine synthetase (EC 2.5.1.6).
GN Name=SMS1;
OS Eleagnus umbellata (Autumn olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Elaeagnaceae; Eleagnus.
OX NCBI_taxID=43233;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root node;
RA Lee S., An C.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit [By similarity].
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AF346305; AAK29409.1; -.
DR HSSP; P13444; 1QM4.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0004478; P:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF02773; S-AdoMet_synth_C; 1.
DR Pfam; PF02772; S-AdoMet_synth_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
SQ SEQUENCE 393 AA; 43096 MW; E6DFFD2A9FAD2347 CRC64;
Alignment Scores:
Pred. No.: 4.8e-146 Length: 393
Score: 1992.00 Matches: 371
Percent Similarity: 98.20% Conservative: 11
Best Local Similarity: 95.37% Mismatches: 7
Query Match: 72.49% Indels: 0
DB: Gaps: 2
US-10-734-698A-38 (1-1485) x Q9AT56 (1-393)
QY 80 GAGACATTCTATTATACCTCAGAGTGAACGAGGGACACCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspAspLeuCyAsp 21
QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGCG 199
Db 22 GlnIleSerAspAlaValLeuAspAlaCyLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGGAACATGCACCAAGACCACTTGGTCATGGCTTCGAGAGATCACCAACCAAGGCC 259
Db 42 CysGluThrCysSerLysThrAenMetValPheGlyGluLeuThrThrLysAla 61
QY 260 AAGCTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAACATCGCTTCTCTCAAC 319
Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgThrIleGlyPheValSerAsp 81
QY 320 GATGTGGACTGATCTGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGAGACGCT 379
Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY 380 GATATTGCCAGGCTGTGCACGCCACCTTACCAGAAAGACCCGAGGAATCGTGCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121
QY 440 GACCAAGGTCACATGTTGGCTATGCCAGCGACGAAACCCCAAGAAATTTGATGCTTGA 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAACTCGTGCTGCTCTCACCGAGGTTCGCAAGAACCACTGCG 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAspGlyThrCys 161
QY 560 CATGTTGTCAGGCTCATCGGAAACCCCAAGTACTGTTGAGTATTACATACACACGCT 619
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAspLysGly 181
QY 620 GCCATGGTTCAGTTCGTCTGCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGAAATTCACCTGACCTCAAGGACATGTCATCAAGCCGTGATCCCGAG 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValValProGlu 221
QY 740 AAGTACCTTGATGAGAAGACCACTTTTCCACTTGAACCCCTCTGCGCTTTGCTCATTTGA 799
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTCAGCGTGATGCTGCTCTCACCGCCGCAAGATCATCATCATCTTACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261
QY 860 TGGGTGCTCATGCTGCTGCTGCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GTGCTTACATTTGAGACAGCGCTGCTAAGACATTGTGGCAAGTGGACTAGCCAGAGG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGCTTATGCCATTGCTGCTGCCGAGCCTTTGCTGCTCTTTGTCAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProAspProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGAGAGATCATGATAGGAGATCTCAACATTTGTGAGGAGAACTTT 1099
Db 322 SerTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341
QY 1100 GATTTTCAGGCGCGGTATGATCTCCATCACTTGATCTCAAGAGGGGTGGGAATAACAGG 1159
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Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41  
QY 200 TGGCAACATGACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAACCAAGGCC 259  
Db 42 CysGluThrCysSerLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AAGCTTGACTACGAGAAGATCGTGGTCGACACCTGACGAGAACATCGGCTTCTCTCAAC 319  
Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
QY 320 GATGTGGGACTTCATGCTGCAACTGCAAGTCTCTGTAAACATTCAGCAGCAGACCCCT 379  
Db 82 AspValGlyLeuAspAlaAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
QY 380 GATATTGCCAGGTTGTCACGCCACCTTTACAAAGACCCGAGGAAATCGGTGTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121  
QY 440 GACCAGGTCACATGTTGGCTATGCCACGGACGAAACCCAGAAATTCATTCAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluTyrMetProLeuSer 141  
QY 500 CATGTTCTTCACTAACTCGTGTCTCGTCTCACCGAGTTCGCAAGAACCGAACCTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CCATGTTGAGGCTGATGGGAAACCCCAAGTGACTGTTGAGTATTACATGACACCGT 619  
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnGluAsnGly 181  
QY 620 GCATGGTTCAGTTCGTCACACTGTCCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAGCAATTCAGTGCATCCCTCAAGGAGCATGTATCAAGCCGCTGATCCCGAG 739  
Db 202 ThrAsnAspGluIleAlaAspLeuLysGluHisValLysProValIleProGlu 221  
QY 740 AAGTACTCTTGATGAGAGACCACTTTCCACTTGACCCCTCTGGCCGTTTGTTCATTGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GTCTCTCAGGTGATGCTGCTCTCACCGCGCAAGATCATATCATCTTACGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTGCTCATGCTGCTGCTGCTCTCCGGAAGATCCCAAGCTTCATAGAGCT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGACAGAGCTGCTAAGAGCATTTGCGCAAGTGCAGCTAGCCAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaAsnGlyLeuAlaArgArg 301  
QY 980 TGCAATGTGCAAGTGTCTTATGCCATGTGTGTCGCCGAGCCCTTGTCTCTTGTGTAC 1039  
Db 302 CysLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCAGCGGAGATCCATGATAGGAGATTCATCAATGTTGAGGAGACTTT 1099  
Db 322 SerTyrGlyThrGlyGlnIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341  
QY 1100 GATTTCCAGGCGCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATACAGG 1159  
Db 342 AspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
QY 1160 TTCTTCAAGACTGCTGCATATGACACTTCGGCAGAGAGGACCTGACTTCATCGGAA 1219  
Db 362 PheLeuLysThrAlaGlyTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db 382 IleValLysProLeuLysTrpGluLys 390

RESULT 7  
METK POPDE  
ID METK POPDE STANDARD; PRT; 395 AA.  
AC P479T6;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
adenosyltransferase) (AdoMet synthetase).  
OS Populus deltoides (Poplar).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC euroids I; Malpighiales; Salicaceae; Populus.  
OX NCBI\_TaxID:3696;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE:Leaf;  
RX MEDLINE=94105359; PubMed=8278561; DOI=10.1104/pp.102.4.1365;  
RA van Doorselaere J., Gielen J., van Montagu M., Inze D.;  
RT "A cDNA encoding S-adenosyl-L-methionine synthetase from poplar.";  
RL Plant Physiol. 102:1365-1366(1993).  
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP.  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
diphosphate + S-adenosyl-L-methionine.  
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -!- PATHWAY: Activated methyl cycle.  
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; M73430; AAA20112.1; .  
CC HSSP; P13444; 1QM4.  
CC InterPro; IPR002133; S-AdoMet\_synt.  
CC Pfam; PF02772; S-AdoMet\_synt\_C; 1.  
CC Pfam; PF02773; S-AdoMet\_synt\_M; 1.  
CC Pfam; PF00438; S-AdoMet\_synt\_N; 1.  
CC PIRSF; PIRSF000497; MAT; 1.  
CC TIGRPFAMs; TIGR01034; metK; 1.  
CC PROSITE; PS00376; ADOLET\_SYNTHETASE\_1; 1.  
CC PROSITE; PS00377; ADOLET\_SYNTHETASE\_2; 1.  
CC ATP-binding; Magnesium; Metal-binding; Multigene family;  
KW One-carbon metabolism; Potassium; Transferase.  
FT NP\_BIND 120 125 ATP (Potential).  
FT METAL 18 18 Magnesium (By similarity).  
FT METAL 44 44 Potassium (By similarity).  
FT METAL 272 272 Potassium (By similarity).  
FT METAL 280 280 Magnesium (By similarity).  
FT BINDING 148 148 ATP (Potential).  
SQ SEQUENCE 395 AA; 43269 MW; 6E90404CE1CD0FCC CRC64;  
Alignment Scores:  
Pred. No.: 8,23e-146 Length: 395  
Score: 1989.00 Matches: 373  
Percent Similarity: 97.95% Conservative: 9  
Best Local Similarity: 95.64% Mismatches: 8  
Query Match: 72.38% Indels: 0  
DB: 1 Gaps: 0  
US-10-734-698A-38 (1-1485) x METK\_POPDE (1-395)

QY 74 ATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACCCCTGACAGCTC 133  
Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20



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QY 134 TCGACCAAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGAGACCCAGACGACGAG 193
Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerIys 40
QY 194 GTTGCTCGCAAAATGACACCAAGACCAACTTTGGTCATGGTCTTCGGAGAGATCACCAACC 253
Db 41 ValAlaCysGluThrCysThrIysThrAsnMetValMetValPheGlyGluIleThrThr 60
QY 254 AAGGCCAACGTTGACTACAGAGAAGATCGTGCCTGACACCTGCGAGAAACATCGGCTTCGTC 313
Db 61 LysAlaAspValAspTyrGluIysIleValArgAspThrCysArgAsnIleGlyPheThr 80
QY 314 TCAAAACGATGCGGACTTCATGCTGACAACTGCAACTGCAAGTCTTGTAAACATTCGAGCAGAG 373
Db 81 SerAlaAspValGlyLeuAspAlaAspAenCysValLeuValAsnIleGluGln 100
QY 374 AGCCCTGATATTGCCAGGGTGTGCACGGCCCACTTACCAAAAGACCCGAGGAAATCGGT 433
Db 101 SerProAspIleAlaGlnGlyValHisGlyHisPheSerLysArgProGluGluIleGly 120
QY 434 GCTGGAGACAGGTCACATGTTGGCTATGTCACAGGACGAACCCAGAAATGTATGCCA 493
Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
QY 494 TTGAGTCATGTTCTGCAACTAACTCGGTGCTCGTCTCACGAGGTTGCGCAAGAACGGA 553
Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysGlnGly 160
QY 554 ACCTGCCCATGTTGAGGCTGATGGGAAACCCAAAGTGACTGTTGAGTATTACATGAC 613
Db 161 ThrCysAlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnGlu 180
QY 614 AACGGTCATGTTCCAGTTCGTGTCACACTGCTTATCTCACCAACATGATGAG 673
Db 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
QY 674 ACTGTCAACCAACGACAAATTCGACGTGACCTCAAGGAGCATGTGATCAAGCGGTGATC 733
Db 201 ThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIle 220
QY 734 CCGAGAAGTACCTTGATGAGAACCAATTTTCCACTTGAACCCCTCGCGCTTTTGTGC 793
Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
QY 794 ATTGAGGTCCTCACGGTATGCTGCTCAGCGGCGGCAAGATCATCATCATCTTAC 853
Db 241 IleGlyGlyProHisGlyLeuSerGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
QY 854 GGAGGATGGGTGCTCATGCTGCTGCTGCTTCTCGGGAAGGATCCCAACCAAGTTGAT 913
Db 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
QY 914 AGGAGTGTGCTTACATTTGTGACAGAGGCTGCTAAAGACATTTGTGGCAAGTGAGTACC 973
Db 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
QY 974 AGAGGTGATTTGTGAAGTCTTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1033
Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
QY 1034 GTTGACACCTATGGCACCGGGAAGATCCCATGATAGGAGATTTCTCAACATTTGGAAGGAG 1093
Db 321 ValAspThrTyrGlyThrGlyLysIleProAspLysGluIleGlnIleValLysGlu 340
QY 1094 AACTTTGATTTGAGGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAT 1153
Db 341 ArgPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
QY 1154 AACAGTTCCTAGACTCTGCATATGACACTTCGGCAGAGAGGACCTCACTTACCA 1213
Db 361 SerArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThr 380
QY 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAG 1243
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Db 381 TrpGluValValLysProLeuLysTrpAsp 390
RESULT 8
Q84MM2 PRELIMINARY; PRT; 393 AA.
AC Q84MM2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosylmethionine synthetase.
GN Name=SAMS;
OS Litchi chinensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Sapindales; Sapindaceae; Litchi.
OX NCBI_TaxID=151069;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-S., Xu X., Huang S.-Z., Fu J.-R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AY259227; AAP13994.1; -.
DR HSP; P13444; 10M4.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet synt.
DR Pfam; PF02772; S-AdoMet synt_M; 1.
DR Pfam; PF00438; S-AdoMet_synt_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase
SQ SEQUENCE 393 AA; 42504 MW; CCB5423C334BEC3 CRC64;
Alignment Scores:
Pred. No.: 1,41e-145 Length: 393
Score: 1986.00 Matches: 370
Percent Similarity: 98.20% Conservative: 12
Best Local Similarity: 95.12% Mismatches: 7
Query Match: 72.27% Indels: 0
DB: 2 Gaps: 0
US-10-734-698A-38 (1-1485) x Q84MM2 (1-393)
QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTGACAAAGCTCTGCCAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAATATCTCCGATGCTGCTCGAGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199
Db 22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGAAACATGCACCAAGACCAACCTTGGTCATGGTCTTCGGAGAGATCACCAAGGCC 259
Db 42 CysGluThrCysThrArgThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAGATCGTGGTGACACCTGCGAGGAACATCGGCTTCGTCTCAAC 319
Db 62 AsnValAspTyrGluGlnIleValArgAspThrCysArgSerIleGlyPheThrSerAsp 81
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QY 320 GATGTGGGACTGATGCTGCAACTGCAAGGTCTCTGTAAACATTGAGCAGCAGCCCT 379  
 Db 82 AspValGlyLeuAspAlaAspAenCysLysValLeuValAenIleGluGlnSerPro 101  
 QY 380 GATATTGCCAGGCTGTGACGCGCCACTTACCAGAGACCCGAGCAATCGGTGCTGGA 439  
 Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121  
 QY 440 GACCAGGTCACATGTTTGGCTATGCCACGAGCAAAACCCAGAAATGTATGTCATTGAGT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCACTAACTCGGTGCTGCTCACCAGAGTTCGCAAGAACGCACTGC 559  
 Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAenGlyThrCys 161  
 QY 560 CCATGTTGAGGCTCATGTTGAAACCCCAAGTCACTGTTGAGTATTACATGACACGGT 619  
 Db 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAenGlyAenGly 181  
 QY 620 GCCATGTTCCAGTTCGTGTCCACTGCTGCTTATCTCCACCAACATGATGAGACTGTG 679  
 Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCAAGCAGAAATTCAGCTGACCTCAGAGGACATGTGATCAAGCCGCTGATCCCGAG 739  
 Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGlnHisValIleLysProValIleProGlu 221  
 QY 740 AAGTACCTTGATGAGAGACCAATTTCCACTTGAACCCCTCGCCGTTTGTTCATTGGA 799  
 Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GGTCTCTCAGCGTGATGCTGCTCACCAGCGCCGCAAGATCATCATCATCTTACGGAGGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
 QY 860 TGGGGTGCTCATGTTGGTGGTCTTTCTCCGGAAGGATCCCAAGAGTTGATAGAGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GTGCTTACATGTGAGCAGCTGCTAGACATGTGCGCAAGTGTGCGCAAGTACCGAAGG 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArg 301  
 QY 980 TGCAATGTGCAAGTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039  
 Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
 QY 1040 ACTATGGCAGCGGGAAGATCCATGATAGGAGATCTCAACATGTGAGGAGAACTTT 1099  
 Db 322 SerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAenPhe 341  
 QY 1100 GATTTCCAGCGCGGTATGATCTCCATCACTGATCTCAAGGGGTGGGAATACAGG 1159  
 Db 342 AspPheArgProGlyMetIleSerValAenLeuAspLeuLysArgGlyAenGlyArg 361  
 QY 1160 TTCTTGAACACTGCTCATATGACACTTCCGAGAGGACCCCTGACTTTCATGAGGAA 1219  
 Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 381  
 QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
 Db 382 ValValLysProLeuLysTrpAspLys 390  
 RESULT 9  
 METK\_LYCES  
 ID METK\_LYCES STANDARD; PRT; 393 AA.  
 AC P43280;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 1) (AdoMet synthetase 1).

GN Name=SAM1;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Rutgers;  
 RX MEDLINE=94289646; PubMed=8018871;  
 RA Espartaco J., Pintor-Toro J.A., Pardo J.M.;  
 RT "Differential accumulation of S-adenosylmethionine synthetase  
 transcripts in response to salt stress.";  
 RL Plant Mol. Biol. 25:217-227(1994).  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 CC 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@sib-sib.ch).  
 CC  
 CC EMBL; Z24741; CAA80865.1; -.  
 DR PIR; S46538; S46538.  
 DR HSP; P13444; 10M4.  
 DR InterPro; IPR002133; S-AdoMet\_synt.  
 DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
 DR Pfam; PF00438; S-AdoMet\_synt\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOLET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOLET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; Multigene family;  
 KW One-carbon metabolism; Potassium; Transferase.  
 FT NP\_BIND 119 124 ATP (Potential).  
 FT METAL 17 17 Magnesium (By similarity).  
 FT METAL 43 43 Potassium (By similarity).  
 FT METAL 271 271 Potassium (By similarity).  
 FT METAL 279 279 Magnesium (By similarity).  
 FT BINDING 147 147 ATP (Potential).  
 SQ SEQUENCE 393 AA; 43301 MW; 81433A565A68039B CRC64;  
 Alignment Scores:  
 Pred. No.: 1.68e-145 Length: 393  
 Score: 1985.00 Matches: 374  
 Percent Similarity: 97.69% Conservativeness: 6  
 Best Local Similarity: 96.14% Mismatches: 9  
 Query Match: 72.23% Indels: 0  
 Db: 1 Gaps: 0  
 US-10-734-698A-38 (1-1485) x METK\_LYCES (1-393)  
 QY 80 GAGACATTCTCTATTACCTCAGAGTCACTGAGGAGGACCCCTGACAGCTCTGCGAC 139  
 Db 2 GluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCCGATGCTGCTCCTCGAGCTTGCCTTGAACAGGACCCACAGCAGGAGTTGCC 199  
 Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValala 41  
 QY 200 TGCAGAACATCGACCAAGACCAACTTGCTGCTATGCTTCTCGGAGAGATCACCACCGAGCC 259  
 Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysala 61



Db 22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluSerLysValAla 41  
QY 200 TCGAAACATGCACCAAGACCACTTGGTTCATGCTCTTCGGAGAGATCACCAACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AAGCTTGACACGAGAGATCGTGGTGACACCTGCGAGAACATCGGCTTCGTCTCAAC 319  
Db 62 AsnIleAspTyrGluLysIleValArgAspThrCysArgGluIleGlyPheValSerPro 81  
QY 320 GATGTGGAGCTTCATGCTGACAACTCAAGTCTTGTAAACATTCAGCAGCAGAGCCCT 379  
Db 82 AspValGlyLeuAspAlaAspAsnCysArgValLeuValAsnIleGluGlnGlnSerPro 101  
QY 380 GATATTGCCAGGGTGTGACGGCCACCTTTACCAAAAGACCCGAGGAATTCGGTGTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
QY 440 GACCAGGTCACATGTTGGCTATGACGAGGAGAAACCCAGAAATGATGCTCATGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTGCACTAACTCGTGTCTCGTCTCACCGAGGTTCCGAGAACCGAACCTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CATGTTGAGGCTCATGAGGAAACCCCAAGTGAAGTGTGAGTATTAATCAATCAACGGT 619  
Db 162 SerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrHisAsnAspAsnGly 181  
QY 620 GCATGGTTCATGCTGTCACACTGTGCTTATCTCCACCCAAACATGATGAGACTGTG 679  
Db 182 AlaMetValProLeuArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAGCAATTCAGTGCATCTCAAGGACATGATCAAGCGGTGATCCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AAGTACTCTGATGAGAGACCAATTTCCACTTCAACCCCTCTGCGCGTGTGTCATGGA 799  
Db 222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCTCAGGTCATGCTGCTCTCACCGCGCGCAAGATCATCATCATCTTACGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTGCTCATGCTGCTGCTTCTCCGGAAGGATCCCAAGCTTGTATAGGACT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGAGACAGGCTGCTTAAGACATTTGCGCAAGTGCAGTACGAGAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301  
QY 980 TGCAATGTCAAGTGTCTTATGCAATGTGTGTCGCGAGCTTGTCTCTCTTGTGAC 1039  
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCAGCGGAGATCCATGATAGGAGATTCATCAATCTGAGAGGACTTT 1099  
Db 322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341  
QY 1100 GATTTCCAGGCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACAGG 1159  
Db 342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuArgGlyGlyAsnGlyArg 361  
QY 1160 TTCTGAAGACTGCTGCATATGACACTTCGGCAGAGAGACCTGACTTCAATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTyrGlu 381  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

## RESULT 11

Q9SBQ7 PRELIMINARY; PRT; 393 AA.  
AC Q9SBQ7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE S-adenosyl-L-methionine synthetase.  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Petunia.  
NCBI\_TaxID=4102;  
RN [1]  
RX SEQUENCE FROM N.A.  
RC TISSUE=Corolla;  
RX MEDLINE=20027448; PubMed=10557255;  
RA Soong S.C., To K.Y.;  
RT "Nucleotide Sequence Of A cDNA (AF170798) Encoding Type I S-Adenosyl-L-Methionine Synthetase From Petunia hybrida. (PGR99-160).";  
RL Plant Physiol. 121:1053-1053(1999).  
CC - FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP (By similarity).  
CC - CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.  
CC - COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and 1 potassium ion per subunit (By similarity).  
CC - PATHWAY: Activated methyl cycle.  
CC - SIMILARITY: Belongs to the Adomet synthetase family.  
DR EMBL; AF170798; AAD48485.1; -.  
DR HSSP; F13444; 1QM4.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR InterPro; IPR002133; S-AdoMet synt.  
DR Pfam; PF02773; S-AdoMet synt C; 1.  
DR Pfam; PF02772; S-AdoMet synt M; 1.  
DR Pfam; PF00438; S-AdoMet synt\_N; 1.  
DR PIRSF; PIRSF000497; MAT; 1.  
DR TIGRFAMs; TIGR01034; metK; 1.  
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
KW Potassium; Transferase.  
SQ SEQUENCE 393 AA; 43169 MW; 0ACDD62F28F6749 CRC64;  
Alignment Scores:  
Pred. No.: 4,92e-145 Length: 393  
Score: 1979.00 Matches: 372  
Percent Similarity: 97.69% Conservative: 9  
Best Local Similarity: 95.38% Mismatches: 9  
Query Match: 72.02% Indels: 0  
DB: 2 Gaps: 0  
US-10-734-698A-38 (1-1485) x Q9SBQ7 (1-393)  
QY 80 GAGACATTCCTATTATTTACCTCAGAGTCAGTGAACGAGGACACCTGACAGCTCTCGGAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGAGCCCGAGACAGAGGTTGCC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
QY 200 TCGGAAACATGCACCAAGACCACTTGGTTCATGCTTCGCGAGAGATCACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AAGCTTGATCTACGAGAGATCGTGGTGCACCTCGAGGAAACATCGGCTTCCTCAAC 319

Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSerAsp 81  
Qy 320 GATGTGGAGCTTGATGCTGACAACTGCAAGGTCCCTGTAAACATTTGACGACGAGCCCT 379  
Db 82 AspValGlyLeuAspAlaAspAnCysLysValLeuValTyrIleGluGlnSerPro 101  
Qy 380 GATATTGCCACGGTGTGACCGCCACCTTACCAAAAGACCCGAGGAATCGGTCTGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysGlnProGluGluIleGlyAlaGly 121  
Qy 440 GACCAAGGTTCATGTTTGGCTATGCCACGACGAAACCCCAAGAAATGATGCAATGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 141  
Qy 500 CATGTTCTTGCAACTAACTCGTCTGCTCTCACCAGGTTGCGAAGACCGAACCTGCG 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy 560 CCATGTTGAGCCTGATGGGAAACCCCAAGTACTGTTGAGTATTACAAATGACACAGCT 619  
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnGluAsnGly 181  
Qy 620 GCCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy 680 ACCAAGCAGAAATTCACACTGACCTCAGGAGCATGTGATCAAGCCGTGATCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaHisAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy 740 AAGTACTCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCGCGCTTTCGATTTGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
Qy 800 GGTCTCACGGTATGCTGCTCTACCGCCCGCAAGATCATCATCTACGACTTACGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
Qy 860 TGGGGTCTCATGGTGGTGTGCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
Qy 920 GGTGCTTACATTTGTGAGACAGCGTCTGAAGACATTTGTCGAAGTGGACTAGCCAGAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaLysSerValValAlaAsnGlyLeuAlaArg 301  
Qy 980 TGCATTGTCAAAGTGTCTATGCCATTGTGTGTCGCCGAGCCTTTGTCTCTTTGTGAC 1039  
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
Qy 1040 ACCTATGGCACCAGGAGATCCATGATAAGGAGATCTCAACATTTGTGAGGAGAACTTT 1099  
Db 322 ThrTyrGlyThrGlyMetIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341  
Qy 1100 GATTTCCAGCCCGGTATGATCTCAACCTTGATCTCAAGAGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
Qy 1160 TTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCCTGACTTCATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspThrAspPheThrTrpGlu 381  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
Db 382 ValValLysProLeuLysCysGluLysAla 391

## RESULT 12

Q944U4  
ID Q944U4 PRELIMINARY; PRT; 395 AA.  
AC Q944U4; (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 26, Last annotation update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE S-adenosyl-L-methionine synthetase.  
GN Name=Sams;  
OS Dendrobium crumenatum (Tropical pigeon orchid)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobieae;  
OC Dendrobium.  
OX NCBI\_TaxID=51096;  
RN [1]\_TaxID=51096;  
RP SEQUENCE FROM N.A.  
RA Han P., Pua E.C.;  
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
CC methionine and ATP (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
CC diphosphate + S-adenosyl-L-methionine.  
CC -!- COPACITOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
CC 1 potassium ion per subunit (By similarity).  
CC -!- PATHWAY: Activated methyl cycle.  
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
DR EMBL; AF420238; AAL16064.1; -.  
DR HSPF; P13444; IQW4.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:000287; F:magnesium ion binding; IEA.  
DR GO; GO:000478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR InterPro; IPR002133; S-AdoMet\_synth.  
DR Pfam; PF02772; S-AdoMet\_synth\_C; 1.  
DR Pfam; PF02773; S-AdoMet\_synth\_N; 1.  
DR PIRSF; PIRSF00497; MAT; 1.  
DR TIGRPFAMs; TIGR01034; metK; 1.  
DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
KW Potassium; Transferase.  
SQ SEQUENCE 395 AA; 43210 MW; 240AA4A7CF8DA440 CRC64;

## Alignment Scores:

Pred. No.: 1.1e-144 Length: 395  
Score: 1974.50 Matches: 370  
Percent Similarity: 97.71% Conservative: 14  
Best Local Similarity: 94.15% Mismatches: 6  
Query Match: 71.85% Indels: 3  
DB: 2 Gaps: 2

US-10-734-698A-38 (1-1485) x Q944U4 (1-395)

Qy 74 ATGGCAGAG-----ACATTCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGAC 127  
Db 1 MetAlaGluValAspThrPheLeuPheThrSerGluSerValAsnGluGlyHisProasp 20  
Qy 128 AAGCTCTCGCACCAATCTCCGATCTCTCTCGACGCTTCCTTGAACAGAGACCCAGAC 187  
Db 21 LysLeuCysAspGlnIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProasp 40  
Qy 188 AGCAAGGTTCCTCGCAACATGACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATC 247  
Db 41 SerLysValAlaCysGluThrCysSerLysThrAsnMetValMetIlePheGlyIle 60  
Qy 248 ACCACCAAGGCCAAGCTTGACTACGAGAAGATCGTGCCTGACACCTCGAGGAACATCCGC 307  
Db 61 ThrThrLysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGly 80  
Qy 308 TTCGTCTCAACAGATGTGGACTTGATGCTGACAACTGCAAGGTCTTTGTAACATTGAG 367  
Db 81 PheValSerAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGlu 100  
Qy 368 CAGCAGACCCCTGATATTGCCAGGGTGTGACGCGCCACCTTACCAGAGACCCGAGAA 427  
Db 101 GlnGlnSerProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGlu 120

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QY 428 ATCGTGCTGGACAGCGGTACATGTTGGCTATGCTACCGACGCAAAACCCAGAAATG 487
DB 121 IIEGLYALAGLYAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeu 140
QY 488 ATGCCATTGAGTCATGCTCTTCAACTAAACCTGGGTCTCGTCTCACCGAGGTGCGCAAG 547
DB 141 MetProLeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLys 160
QY 548 AACGGAACCTGCCATCGCTTGGAGCCCTGATGGGAAACCAAGTGAAGTCTGTGAGTATTAC 607
DB 161 AsnGlyThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrArg 180
QY 608 AATGACAACGGTCCCATGTTCCAGTTCAGTTCGTGTCACACATGCTGTATCTCCACCCCAAT 667
DB 181 AsnAspGlyGlyAlaMetValProIleArgValHisThrValLeuIleSerThrGlnHis 200
QY 668 GATGAGACTGTGACCAACGACGAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCG 727
DB 201 AspGluThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysPro 220
QY 728 GTGATCCCGAGAGTACCTTGTATGAGAAGACCATTTTCCACTTGAACCCCTCTGCGCCT 787
DB 221 ValValProGluGlnTrpLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArg 240
QY 788 TTTGTCATTGAGAGTCTCTCAGGTGATGCTGTCTCACCAGCGCGCAAGATCATCATGAT 847
DB 241 PheValIleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAsp 260
QY 848 ACTTACGAGGAGTGGGTCTCATGTTGGTGTGCTTCTCCGGAGGATCCCAACCCAG 907
DB 261 ThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLys 280
QY 908 GTTGATAGAGTGGTCTTACATTTGTGACAGAGGTGCTTAAGAGCATTTGTGCAAGTGA 967
DB 281 ValAspArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaSerGly 300
QY 968 CTAGCCAGAGTGTGATTGTCAGGCGCGGTATGATCTCCATCAACTTGAATCTCAAGAGGGT 1147
DB 301 LeuAlaArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSer 320
QY 1028 GTCCTTTGTGACCTATGCGACCGGAGATCCATGATAGAGAGTCTTCAACATTTGG 1087
DB 321 ValPheValAspThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleVal 340
QY 1088 AAGGAGAACTTTGATTTCAGGCGCGGTATGATCTCCATCAACTTGAATCTCAAGAGGGT 1147
DB 341 LysGluAsnPheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGly 360
QY 1148 GGAATAACAGTCTTCAAGTCTGCTGATATGACACTTCCGAGAGAGGACCCCTGAC 1207
DB 361 Gly---AsnArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAsp 379
QY 1208 TTCACATGGGAAGTGTGTCAGGCCCTCAAGTGGGAGAG 1246
DB 380 PheThrTrpGluValLysProLeuLysTrpAspLys 392

RESULT 13
Q8GTL5 PRELIMINARY; PRT; 429 AA.
AC Q8GTL5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE S-adenosylmethionine synthase.
GN Name=SAMS;
OS Carica papaya (Papaya).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Caricaceae; Carica.
OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ripening fruit mesocarp;
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RA Kasazlinda J., Chong J.Y., Othman R., Ali Z.M., Lazan H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine -> phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AF531479; AAN07179.1; -.
DR HSSP; P13444; 1QM4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF02773; S-AdoMet_synth_C; 1.
DR Pfam; PF00438; S-AdoMet_synth_M; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGSFAM; TIGSF01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
SQ SEQUENCE 429 AA; 47085 MW; 905E68EA23F37112 CRC64;

Alignment Scores:
Pred. No.: 1.62e-144 Length: 429
Score: 1972.50 Matches: 381
Percent Similarity: 89.04% Conservative: 17
Best Local Similarity: 85.23% Mismatches: 26
Query Match: 71.78% Indels: 23
DB: 2 Gaps: 4

US-10-734-698A-38 (1-1485) x Q8GTL5 (1-429)
QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTAACGAGGACACCCCTGACAGCTCTGCGAC 139
DB 2 GlnThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTGCC 199
DB 22 GlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGGAAACATGCACCAAGACCAACTTGTGTCATGCTTCCGAGAGATCACCAAGGCC 259
DB 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGGTCACACCTGCAGAACATCGCTTCTGCTCTCAAC 319
DB 62 AspValAspTyrGluLysIleValArgAspThrCysArgSerIleGlyPheValSerAsp 81
QY 320 GATGTGGACTTGTATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAGACCCCT 379
DB 82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnSerPro 101
QY 380 GATATTGCCAGGGTGTGCAGCGCCACTTACCAAAAGACCCGAGGAATATCGGTCTGA 439
DB 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121
QY 440 GACCAGGTCATGTTTGGTGTATGCCACGACGAGAAACCCCAAGATTTGATGCTTGA 499
DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAAACTCGTCTGCTCTCACCGAGGTTTCGAAGAACGGAACCTG 559
DB 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
QY 560 CCATGTTGAGCCCTGATGGGAAACCCCAAGTACTGTTGAGTATTACATGACACCGT 619
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Db      162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyraenGluAenGly 181
Qy      620 GCATGGTTCAGTTCGTCGTCACACTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db      182 AlaArgValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
Qy      680 ACCAAGCAGCAATTCGACCTCACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739
Db      202 ThrAsnAspGluLeuAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 221
Qy      740 AAGTACCTTGATGAGAAGACCAATTTTCCATTTGAACCCCTCTGGCCGTTTGTTCATGGA 799
Db      222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
Qy      800 GGTCTCAGCGTATGCTGCTCTACCCGCCGACAGATCATCATGATCTTACCGAGA 859
Db      242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261
Qy      860 TGGGGTGCTCATGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGT 919
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
Qy      920 GTGCTTACATTTGAGCAGAGCTGCTAAGACATTTGTGGCAAGTGGACTAGCCAGAAGG 979
Db      282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
Qy      980 TGCATTTGTCAGTGTCTTATGCCATTTGGTGTGCCGAGCCCTTCTGCTCTTTGTTGAC 1039
Db      302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValTyrValAsp 321
Qy      1040 ACCTATGGCAGCGGAAGATCCATTAAGGAGATTTCTCAACATTTGTGAAGGAGAACTTT 1099
Db      322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341
Qy      1100 GATTTACAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATTAACAGG 1159
Db      342 AspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGlyGlyAsnSerArg 361
Qy      1160 TTCTTTGAGACTGCTGCATATGGACATCTCGCAGAGGAGCCCTGACTTCACATGGGAA 1219
Db      362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381
Qy      1220 GTGGTCAAGCCCTCAAGTGGGAGAGCGCTAAGGCCATTTCTATCCACTGCAATGTGCTG 1279
Db      382 ValValLysProSerSer-----GlyArgSerLeuAsnLeuLysValLeu 396
Qy      1280 GGAGTTTTTTAGGTTGGCCCTTATAATGTCTATTATCCATAACTTTCCAGTCCCTTGT 1339
Db      397 ValValIle-----IlePro 401
Qy      1340 CTGTGTTTT--TCTCTGTCGTC-----CTCCTCCTATTTTGTCTCTGCTTCA 1390
Db      402 AlaCysPheIleGluLeuIleGlyCysLeuMetLeuMetLeuAsnSerProTyrSer 421
Qy      1391 TTTGTAATTTTACATGATC 1411
Db      422 IleGluValSerTyrMetMet 428

RESULT 14
Q6GV10 PRELIMINARY; PRT; 393 AA.
AC Q6GV10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE S-adenosyl methionine synthase.
OS Solanum brevident.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4115;
RN [1]
RP SEQUENCE FROM N.A.
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RC      TISSUE=Leaf;
RA      Seo H.W., Yi J.Y., Moon J.Y., Park Y.E., Cho J.H.;
RL      Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC      methionine and ATP (By similarity).
CC      -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC      diphosphate + S-adenosyl-L-methionine.
CC      -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC      1 potassium ion per subunit (By similarity).
CC      -!- PATHWAY: Activated methyl cycle.
CC      -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR      EMBL; AY635050; AAT47716.1; -.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0000287; F:magnesium ion binding; IEA.
DR      GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR      InterPro; IPR002133; S-AdoMet synt.
DR      Pfam; PF02773; S-AdoMet synt_C; 1.
DR      Pfam; PF00438; S-AdoMet_synt_N; 1.
DR      PIRSF; PIRSF000497; MAI; 1.
DR      TIGRFS; TIGR01034; metK; 1.
DR      PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
DR      PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
KW      ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW      Potassium; Transferase.
SQ      SEQUENCE 393 AA; 43235 MW; 653F7337FBEE9C56 CRC64;

Alignment Scores:
Pred. No.: 3.53e-144 Length: 393
Score: 1968.00 Matches: 370
Percent Similarity: 97.42% Conservative: 8
Best Local Similarity: 95.36% Mismatches: 10
Query Match: 71.62% Indels: 0
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x Q6GV10 (1-393)
Qy      80 GAGACATCTCTATTACTCAGTCACTGAGGACACCTGACAGCTCTGCGAC 139
Db      2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysasp 21
Qy      140 CAATCTCCGATGCTGCTCGACGCTTGCCTTCAACAGGACCCAGACAGCAAGTTGCC 199
Db      22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
Qy      200 TGCAGAACATCCACCAAGACCAACTTGTCTATGTTCTCGAGAGATCACCACCAAGGCC 259
Db      42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61
Qy      260 AACGTTGACTACGAGAGATCGTGGTGACACCTGCAGGACATCGGCTTCTCAAC 319
Db      62 IleValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsp 81
Qy      320 GATGTGGGACTTGATGTCACAACTGCAAGTCTCTTTAAACATTTGACAGCAGACGCT 379
Db      82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnGlnSerPro 101
Qy      380 GATATTGCCAGGTGTGCACGCCACCTTACCAGAGACCCGAGGAAATCGGTGCTCGA 439
Db      102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121
Qy      440 GACCAAGGTTCATGTTGGCTATGCCACGACGAAACCCAGACATTCGATCCCATGAGT 499
Db      122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
Qy      500 CATGTTCTTCAACTAAACTCGGTCTCGTCTCACCCAGAGTTTCGCAAGACCGAACCTGCG 559
Db      142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
Qy      560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGATGATTATCAATGACACCGGT 619
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Db 162 ArgTrpLeuLysProAspGlyLysThrGlnValThrValGluTyrCysAsnAspAsnGly 181
Qy 620 GCCATGTTCCAGTTCGTGTCACACATGCTCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
Qy 680 ACCAACGACAAATTCGACGTGACCTCAAGGACATGTGATCAAGCGGTGATCCCGGAG 739
Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisAlaIleLysProValIleProGlu 221
Qy 740 AAGTACCTTGATGAGAAGACCATTTTCCACTTCAACCCCTCTCGCGCTTTGTGCTTGA 799
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
Qy 800 GGTCTCTACAGTGTGATCTGTCTCACCGCGCCGAAGATCATCATCATCTTACGGAGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261
Qy 860 TGGGGTCTCATGTTGGTGGTGTCTTCTCGGGAAGGATCCCAACCAAGTTGATGAGGT 919
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
Qy 920 GGTGCTTACATCTGTGAGACAGGCTGTAGAGCATTTGTGCAAGTGTGCAAGTGTGCAAG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301
Qy 980 TGCAATTGTCAAGTGTCTTATGTCATTGTGTGTCGCCGAGCTTTGTCTGTTGTGAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
Qy 1040 ACCTATGGACCGGGAAGATCCATGATATAGGAGATTCTCAACATTTGGAAGGAACTTT 1099
Db 322 ThrTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341
Qy 1100 GATTTCAGGCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGATACAGG 1159
Db 342 AspPheArgProGlyMetSerIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361
Qy 1160 TTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGACCTGACTTCAATGGGAA 1219
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrpGlu 381
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAG 1243
Db 382 ValValLysProLeuLysTrpGlu 389

RESULT 15
Q9FUZ1 PRELIMINARY; PRT; 393 AA.
AC Q9FUZ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosylmethionine synthetase.
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu J.-Z., Pua E.-C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the Adomet synthetase family.
CC EMBL; AF211220; AAG17666.1; -.
DR HSSP; P13444; 1QM4.
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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000287; F:magnesium ion binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-Adomet synt.
DR Pfam; PF02773; S-Adomet synt_C; 1.
DR Pfam; PF02772; S-Adomet synt_M; 1.
DR Pfam; PF00438; S-Adomet synt_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
SQ SEQUENCE 393 AA; 42879 MW; 65BDAC0A52576122 CRC64;
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## Alignment Scores:

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Pred. No.: 1.48e-143 Length: 393
Score: 1960.00 Matches: 367
Percent Similarity: 97.94% Conservative: 14
Best Local Similarity: 94.34% Mismatches: 8
Query Match: 71.32% Indels: 0
DB: 2 Gaps: 0
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US-10-734-698A-38 (1-1485) x Q9FUZ1 (1-393)

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Qy 80 GAGCATTTCCCTATTATTACCTCAGAGTCAGTCAACGAGGACACCCCTGACAGAGCTCTGGAC 139
Db 2 GluserPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
Qy 140 CAAATCTCCGATGTCTCTCGACGCTTGCCTTGAACAGGACCCACAGACAGCAAGGTGGC 199
Db 22 GlnIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
Qy 200 TCGGAAACATGCACCAAGACCAACTTGTGTCTATGTCATGTCGAGAGATCACCAACAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
Qy 260 AACGTTGACTACGAGAGAGATCGTGGTCACACCTGCGAGAACCTCGCTCTCAAC 319
Db 62 AsnValAspTyrGluLysIleValArgGluThrCysArgGluIleGlyPheIleSerAsp 81
Qy 320 GATGTGGGACTTGATGTCACAACTGCAAGCTCTTTGTAACATTGAGCAGCAGAGCCCT 379
Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 101
Qy 380 GATATTGCCAGGTGTGCACGGCCACTTACCAAAAGACCCGAGGAATCGGTCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121
Qy 440 GACCAAGGTTCATGTTTGGCTATGCCACGACGAGAACCCCAAGATTCATGCCATTGAGT 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
Qy 500 CATGTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACCGAACCTGC 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnGlyThrCys 161
Qy 560 CCATGTTGAGCGCTGATGGGAAACCAACCAAGTGAAGTGTGATGATTTACATGACACACGGT 619
Db 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrPheAsnGluAsnGly 181
Qy 620 GCCATGTTCCAGTTCGTGTCACACTGTGTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
Qy 680 ACCAACGACAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCGGAG 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysIleValIleLysProValIleProGlu 221
Qy -740 AAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGCGCGCTTTGTGCTTGA 799
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Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCTACGGTGTGCTGTCTACCGGCCCAAGATCATCATCTTACGGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGGTGTCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACAAGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTGTGAGACAGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArg 301  
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCTTGTCTGTCTTGTGTTGAC 1039  
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCACCGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGACTTT 1099  
Db 322 SerTyrGlyThrGlyLysIleProAspLysGluIleLeuGluIleValLysGluSerPhe 341  
QY 1100 GATTTCAAGCCCGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
QY 1160 TTCTTGAAGACTGTGTCATATGGACACTTCGGCAGAGAGGACCCCTGACTTCAATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAAG 1246  
Db 382 ValValLysProLeuLysSerAsnLys 390

Search completed: August 25, 2005, 17:24:26  
Job time : 298.5 secs